



ATPT2	: ---MES---LSSSLVSAAGG---FCWKKQN---LKLHSLSEIRVLRCDSKVVAKPK---FR---NNLVRP---DGQG	: 59
ATPT3	: MAFFGLSRVSRRLKSSVSVPSSSSALLOQKHSLSPVTHYTNPFKCYPSWNDNYQVWSKREHQEKEFGVGWNYRLICGMSSS	: 90
ATPT4	: ---MWRRS---VYRFSSRISSVSSLPNRLIPWSREL---CAVNSSESPPVSTESTAKLGITGV---RSD---ANRVFA---ATA	: 69
ATPT8	: ---MVLAEVPKLAS---AAEYFFKR---GVOGKQFR---STILLMATA---LN---VRVPE---ALIG	: 48
ATPT12	: ---MTS---LNNVSTIHSRVTSVDRGVLSLRN---SDSVEFTRRR---SGFSULIYESPCR---REV---VRAAE---TDED	: 64
ATPT2	: SLLLYP---KHKSRRFVNATAGQPEAFDSNSKQKSFDRDSDAFYRFSR---PHTVIGTVLSILSVSLAVEKVSDDISPLFTGILEA	: 141
ATPT3	: SVLEGKPKKDDKEKSDGVVKKASWDDLYLPEEVRGYAKLARLDKPHGTWLLAWPCMWSTAL-AADPGSLPSF--K-----YMAIFGCG	: 171
ATPT4	: AATATAT---TG-EISSRVAALAGLGHYARCWELSK-AKLSMLVATS---GTGKTEGT-GNAALISFPGL-----C-YTCA	: 137
ATPT8	: ESTDIVT---SELVRQRGIAEITEMIHVASLLHDDVL-DDADTRRGVGS---LNVVGNKMSVLAGDFFLLS-----RACG	: 117
ATPT12	: KVKSQTE---DKAPAGGSSINQLLGKKG-ASQETNKKIRLQITKPV-TWP---PLVWGVVCGAAASGNFHWTPED-----VAKSILCM	: 140
ATPT2	: VVAALMMNIYIVGLNQLSDVEIDKVNKP---YLPLASGEYSVNTGIAIVASFMSMS-FWLGWIVGSGWPLFWA---LFVSMFLGTANINL	: 224
ATPT3	: AL---LRGAGCTINDLEODIDTKVDRTKLRPIASCLTTPFGICGQLLGL-LGILLQNNYS-----RVLGASSLLLVESY	: 248
ATPT4	: GT---MMLAASANSINQLFEISNDSKMKRTMLRPLSPGRTSVPHAWATATAGASCACLLASKTNMLAAG-----LASANLVLYAFVATP	: 219
ATPT8	: AL---AALKNTEVVALLATAMEHLVTGET---MEITSTEORYSMDYNNQKTYKT---ASLSNSCK-----AVAVLTGQTAEVAV	: 190
ATPT12	: MMSGPQLTGTYQTINDWYDRDIDAINEP---YRPISCAISEPEVITQVWVLLTGG-LGAGLVDVWAGHTTPTVTFYALGGSLLSVLYSA	: 227
ATPT2	: PLTRWKRFAVAAMCITAVRAITVQIAFYLHIQTHVFGRPILFTRPIIFATAFMSFFS-VVIAAFKIDIPDTEG-----D-----KI	: 299
ATPT3	: P---MKRFTFWPQAFGLT---INWGALLGWT---AVKGSFAPSIVEP---LYLSGVCWTLVYDTHYAHQDKED-----D-----VK	: 314
ATPT4	: LKQLHPINTWVGAVV---GATPPILGMA---AASGQISYNSMTTPAALYFWQPHFMALAHLCRNDAAGGYKMLSLFDPGKRIAA	: 300
ATPT8	: LAFEYGRNLGLAFQLI---DDIDDFTGTS---ASLGKGSLSDIRHGVIIPILFAMEEFPQIREVVDQVEK-----DP-----RN	: 259
ATPT12	: PPKLKLKONGVGNFA-LG---ASYSLPWVWAGQ---AATFGTTPDVVVT---LLLYSTAG-LGIAVNDFKSVEG-----D-----RA	: 294
ATPT2	: FGIRS---FSVTLGQ---KRVFWTC---VTELOMAYAVAILVGTSPFPWSK---MISVVGHVTLATTLWARAKSVDLSSKTEITSCN	: 375
ATPT3	: VGVKS---TALREFGD---NKKLWLTGFGHASICGFIASGFSADLGWQYVAS---LAAASGQLGWLQIGTADLSSGADCSRKFVSNKWF	: 392
ATPT4	: VALRNCFYMIPLGFIAYDWGLTSSWFQLESTLTLAATAFSFYRDRTHKARKMFHASLFLPVEFMSGLLLHRVSNNDNQQLVEEAGL	: 390
ATPT8	: VDIAL---EYLGKSK---GQQ---RARELAMEHANLAAANAIGSPET---DNEDVKRSRRALIDLTHRVITRNK-----	: 321
ATPT12	: LGLOS---LPVAFGT---ETAKWTC-VGADITQLSVAGYLLASGKPYMALA-LVALTIPQIVFQFKYFLKDPVKYDVKYQASAOPE	: 373
ATPT2	: -MFIWKLFYAE---YLLLPFLK-----	: 393
ATPT3	: GAIIFSGVVLG---RSFQ-----	: 407
ATPT4	: TNSVSGEVKTQRRKRVAQPPVAYASAFPFLPAPSFYSP	: 431
ATPT8	: -----	: -
ATPT12	: -LVLGIFVTA---LASQH-----	: 387

Figure 1

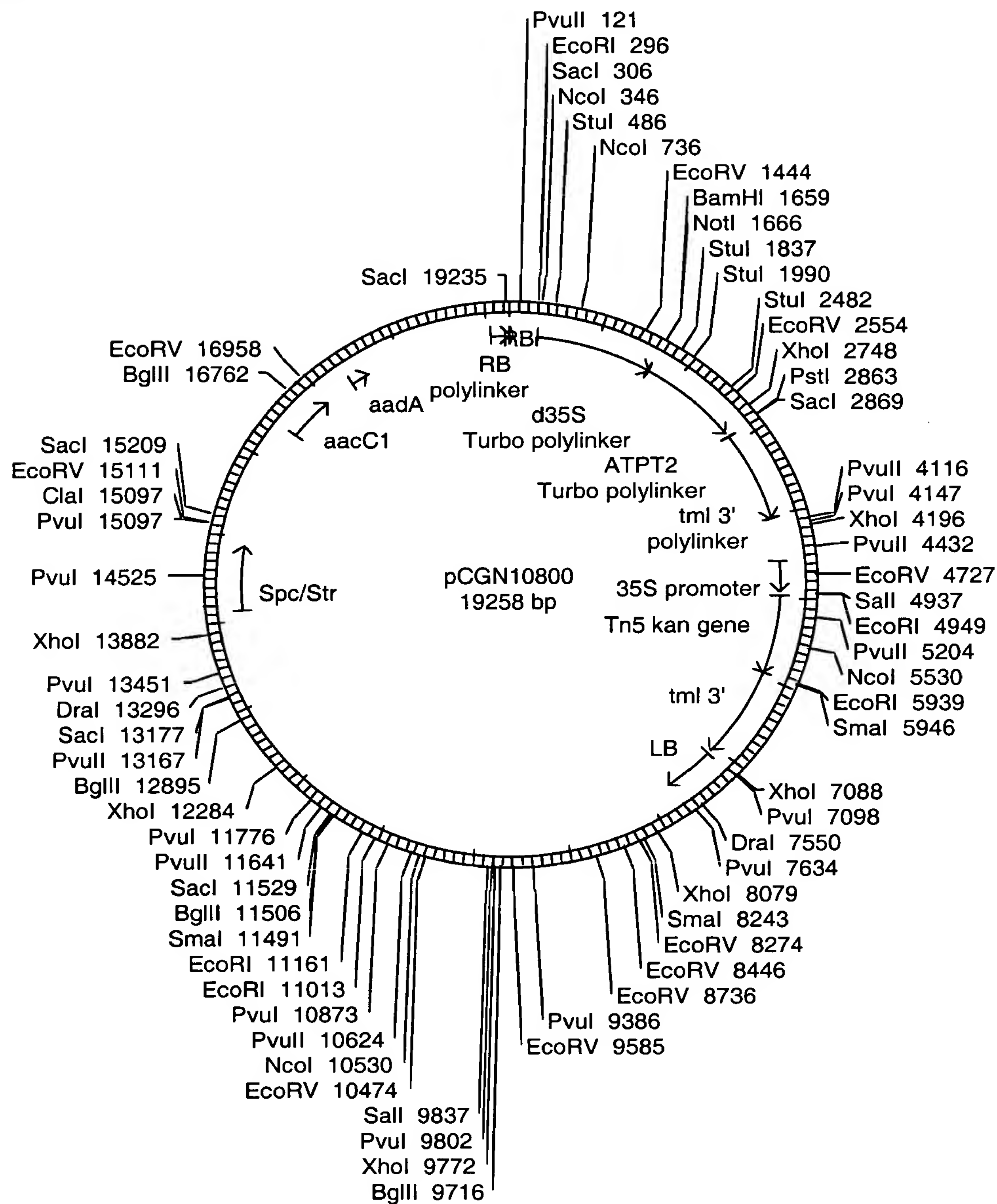


Figure 2

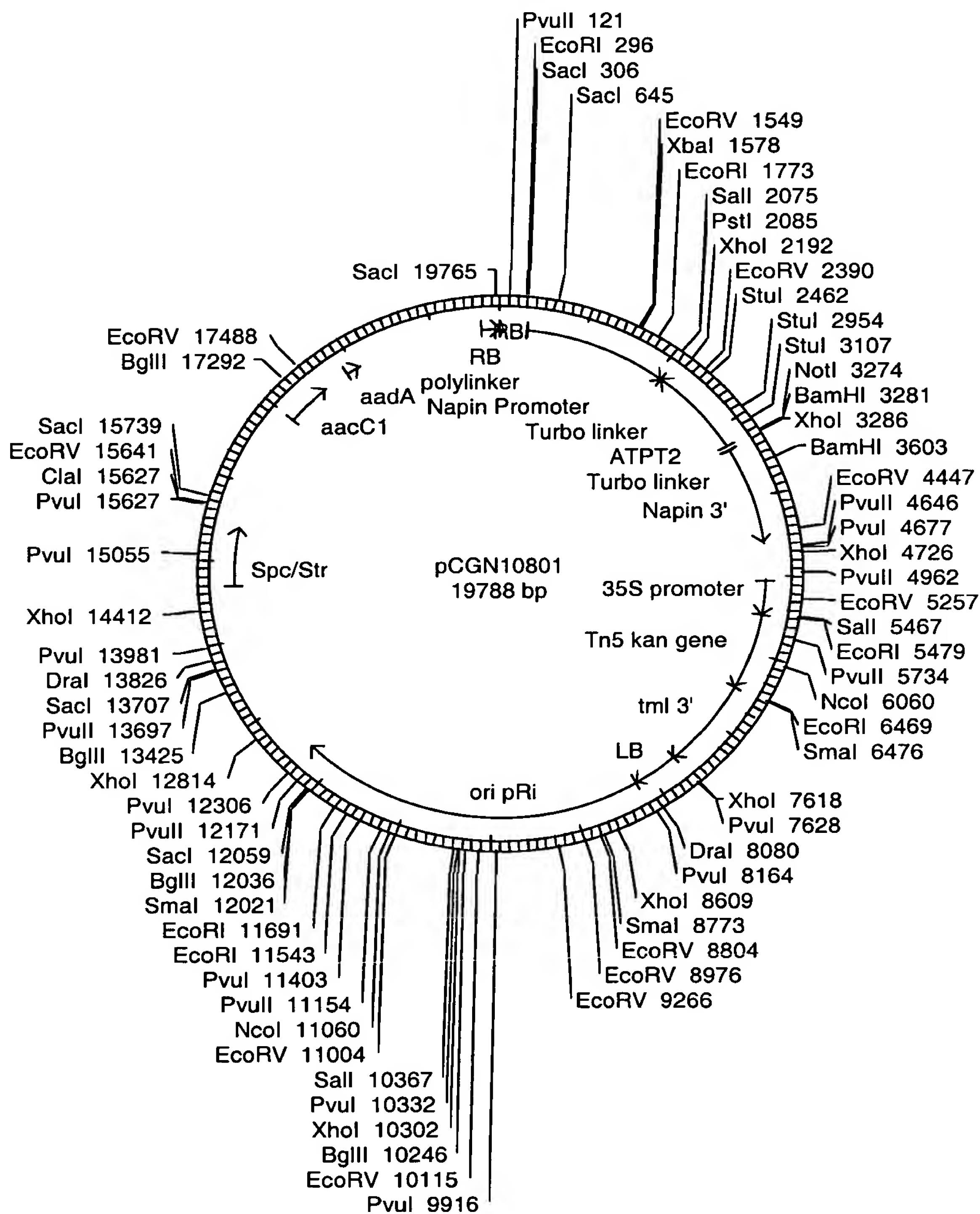


Figure 3

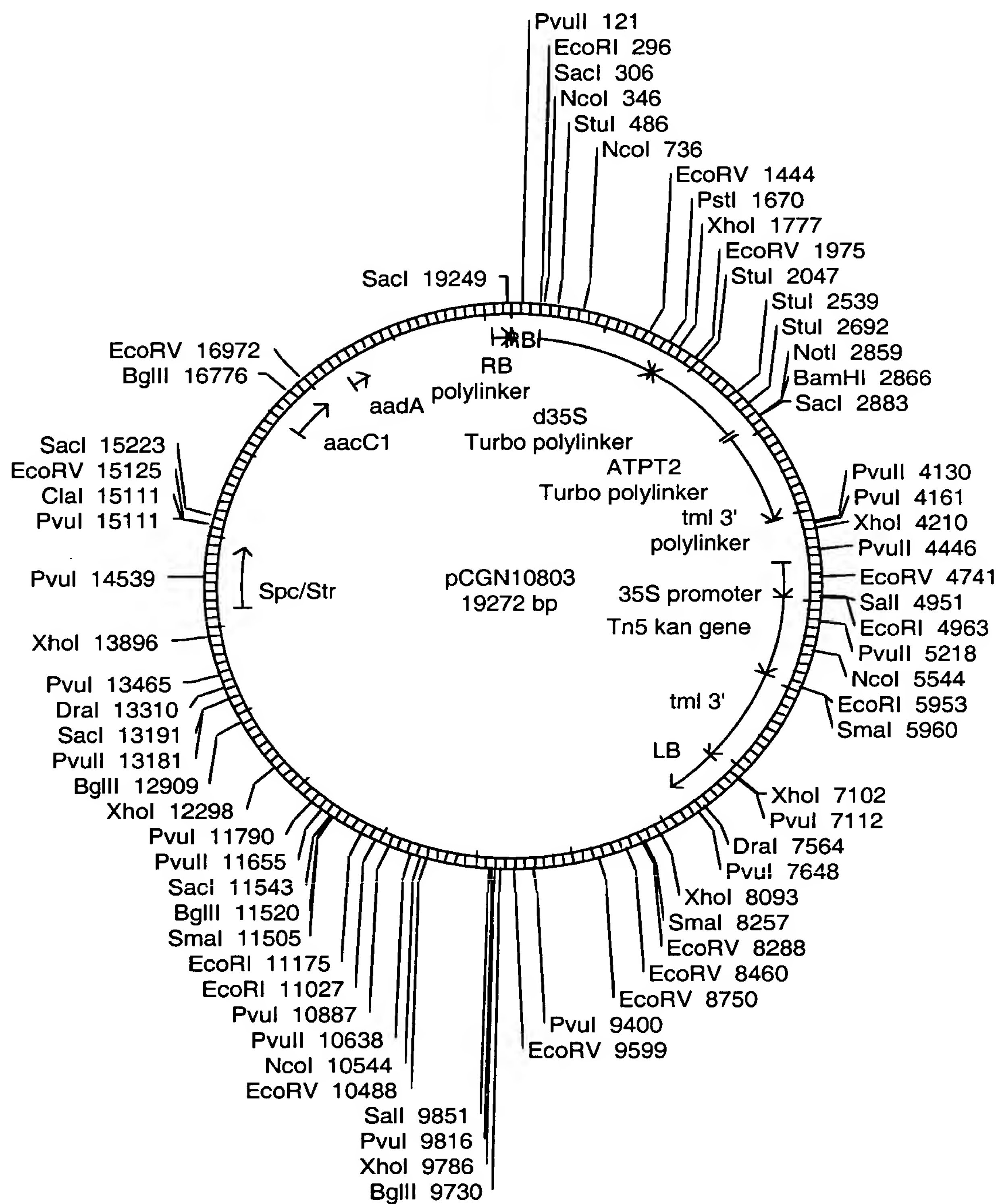


Figure 4

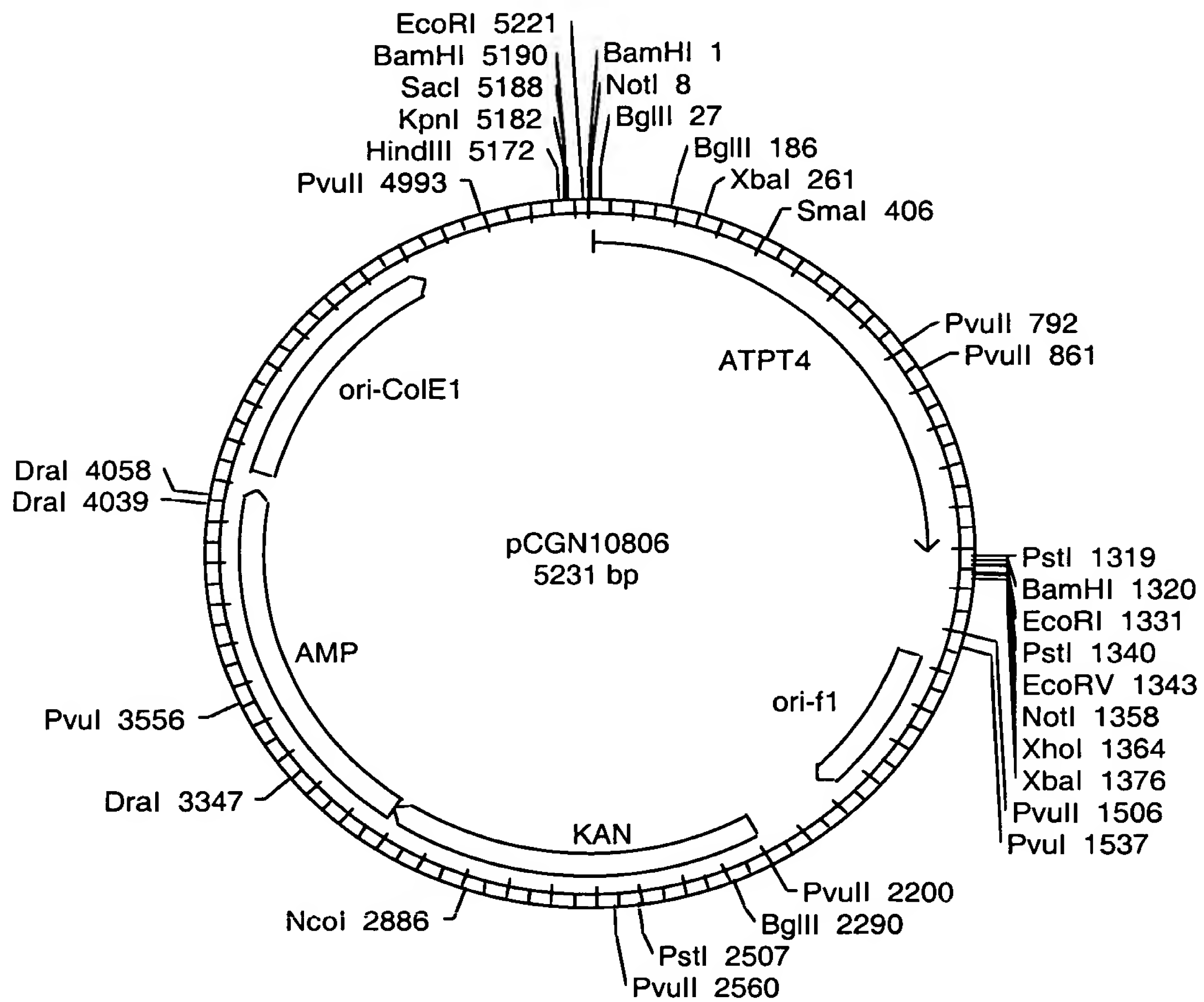


Figure 5

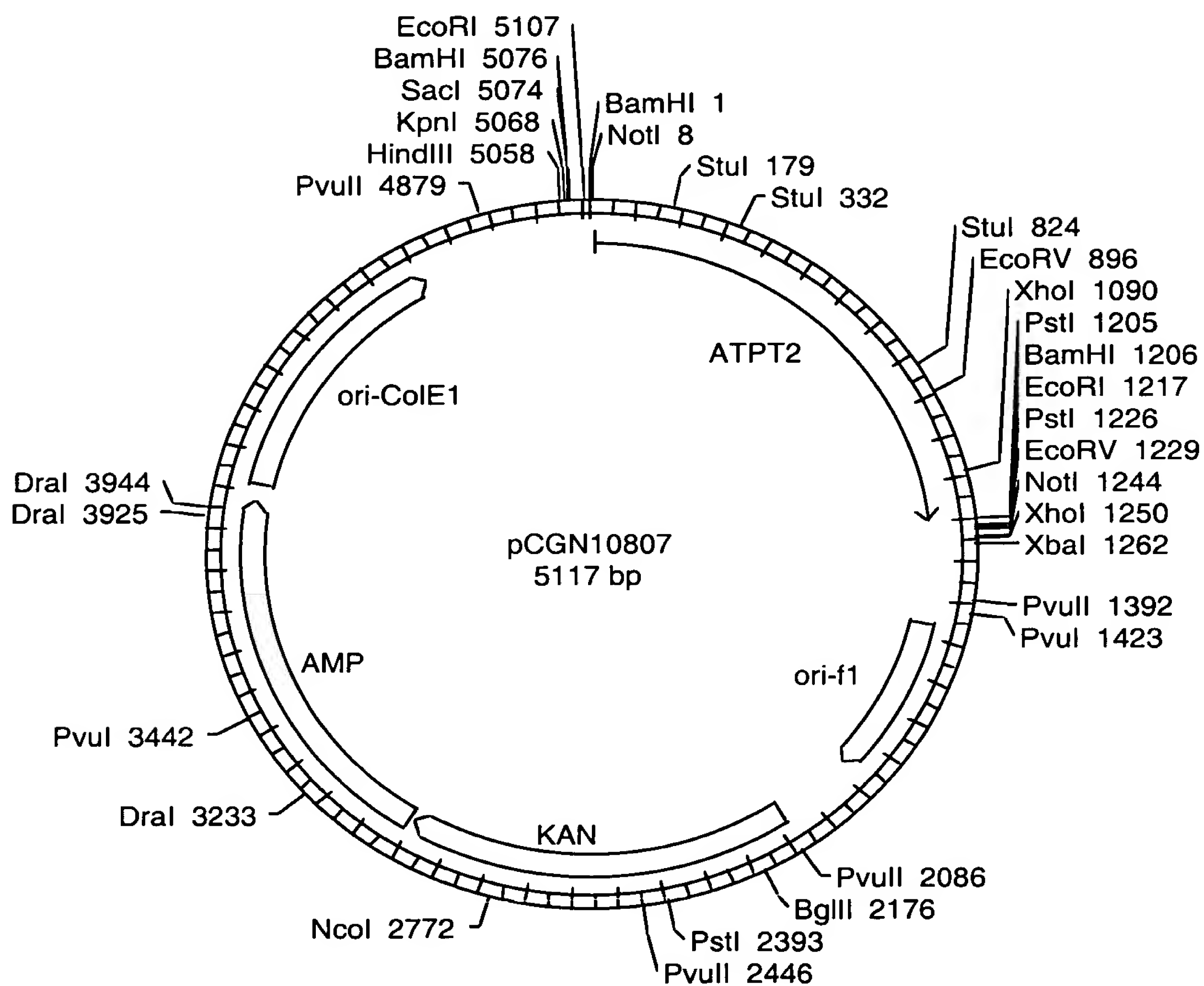


Figure 6

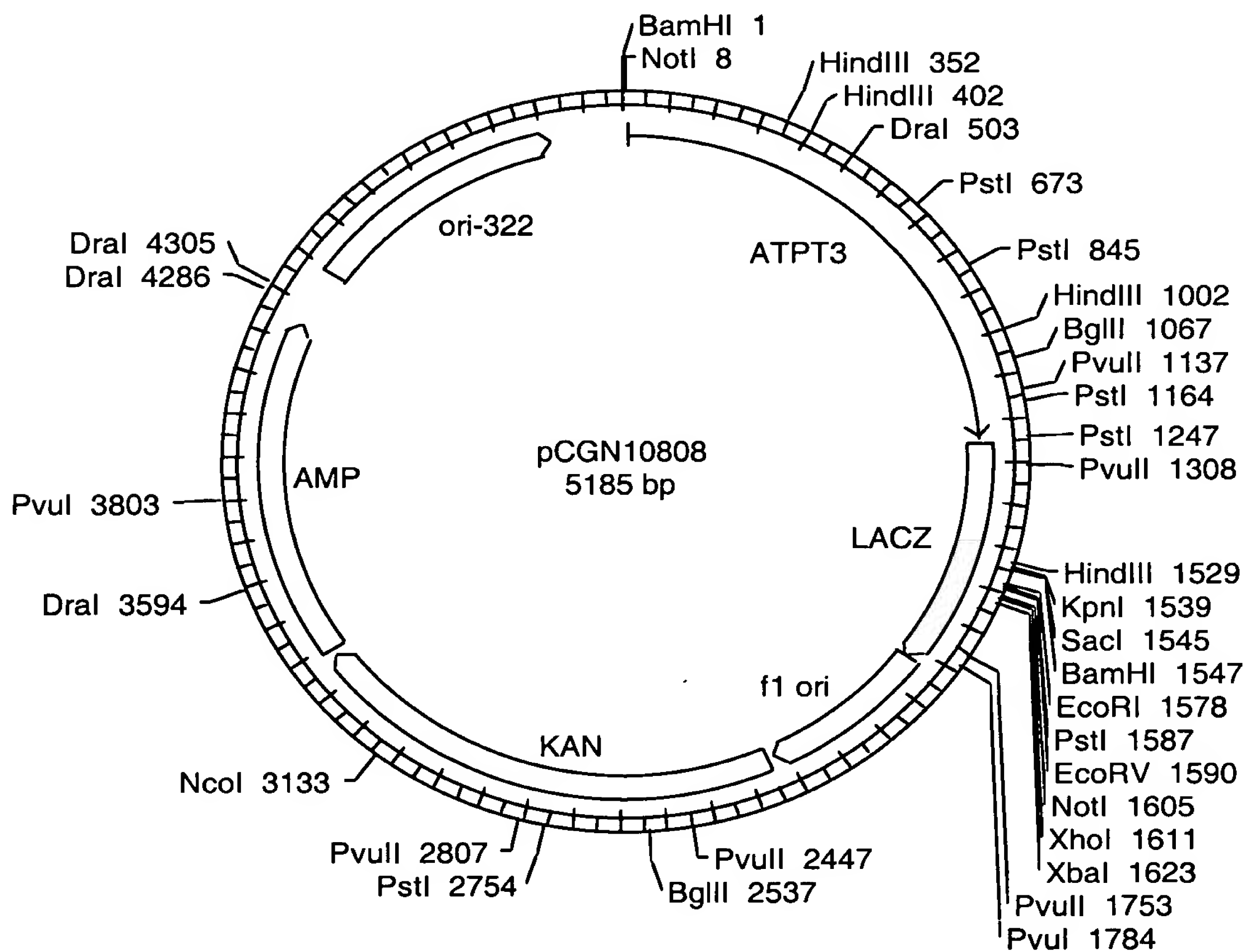


Figure 7

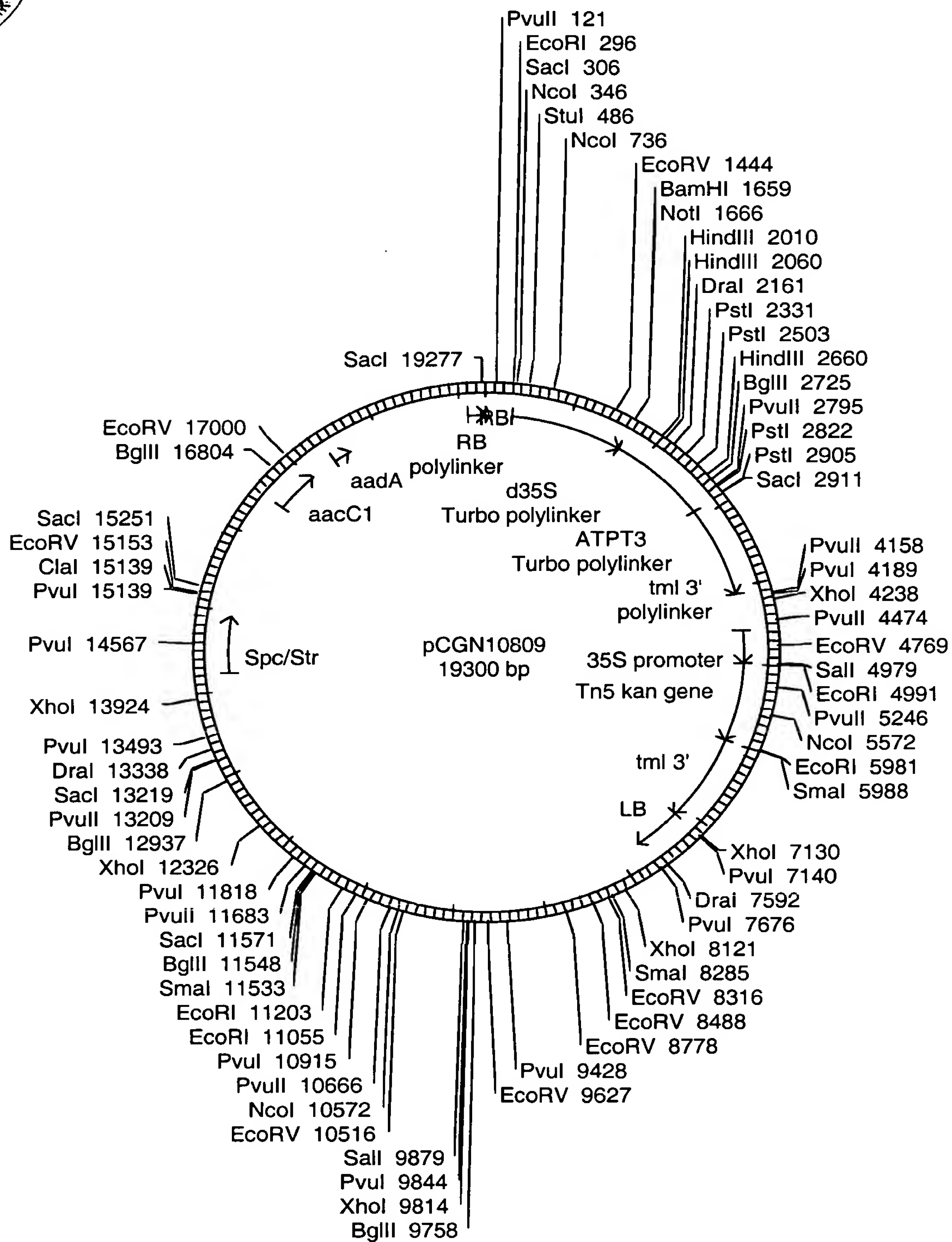


Figure 8

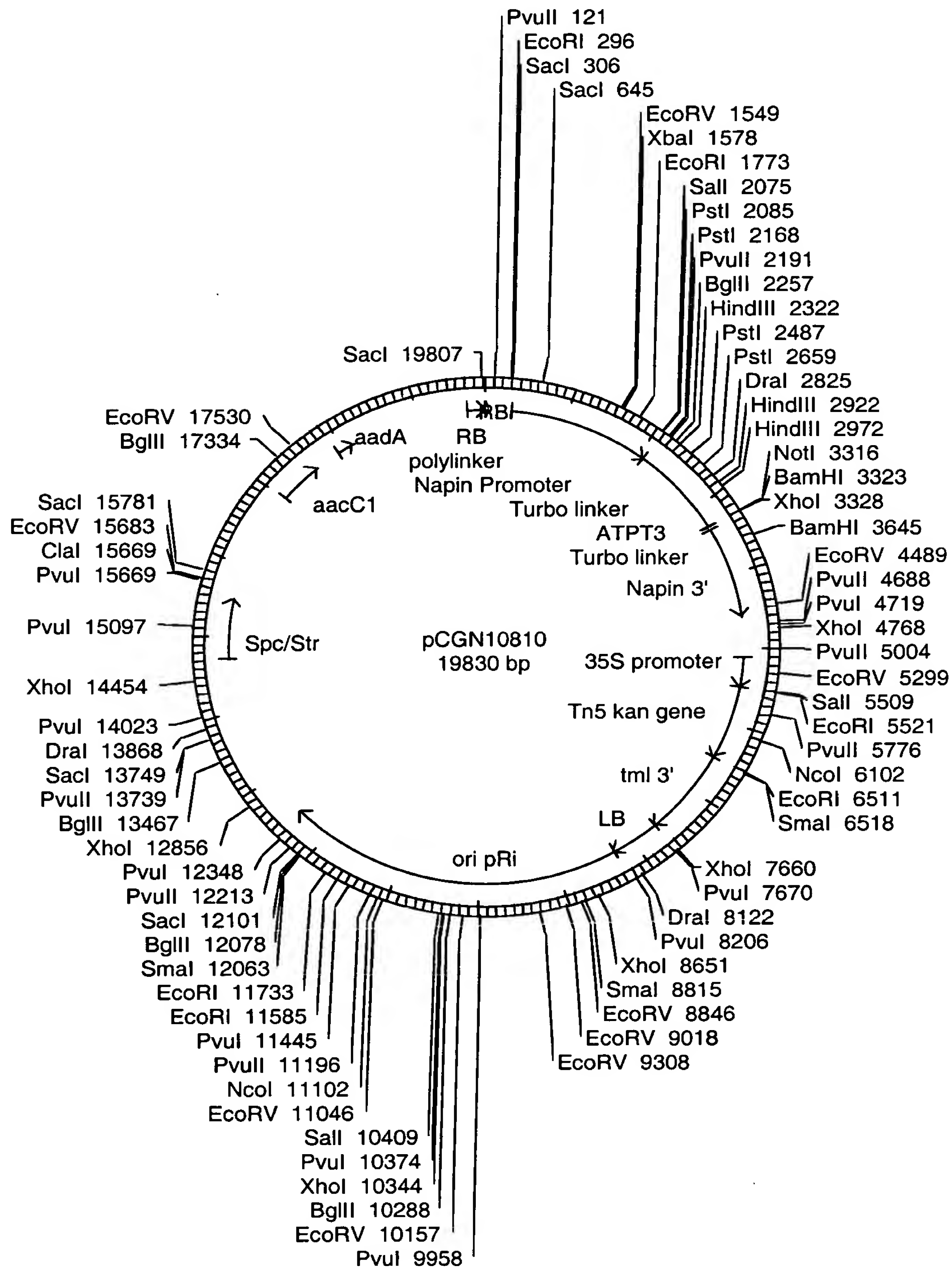


Figure 9

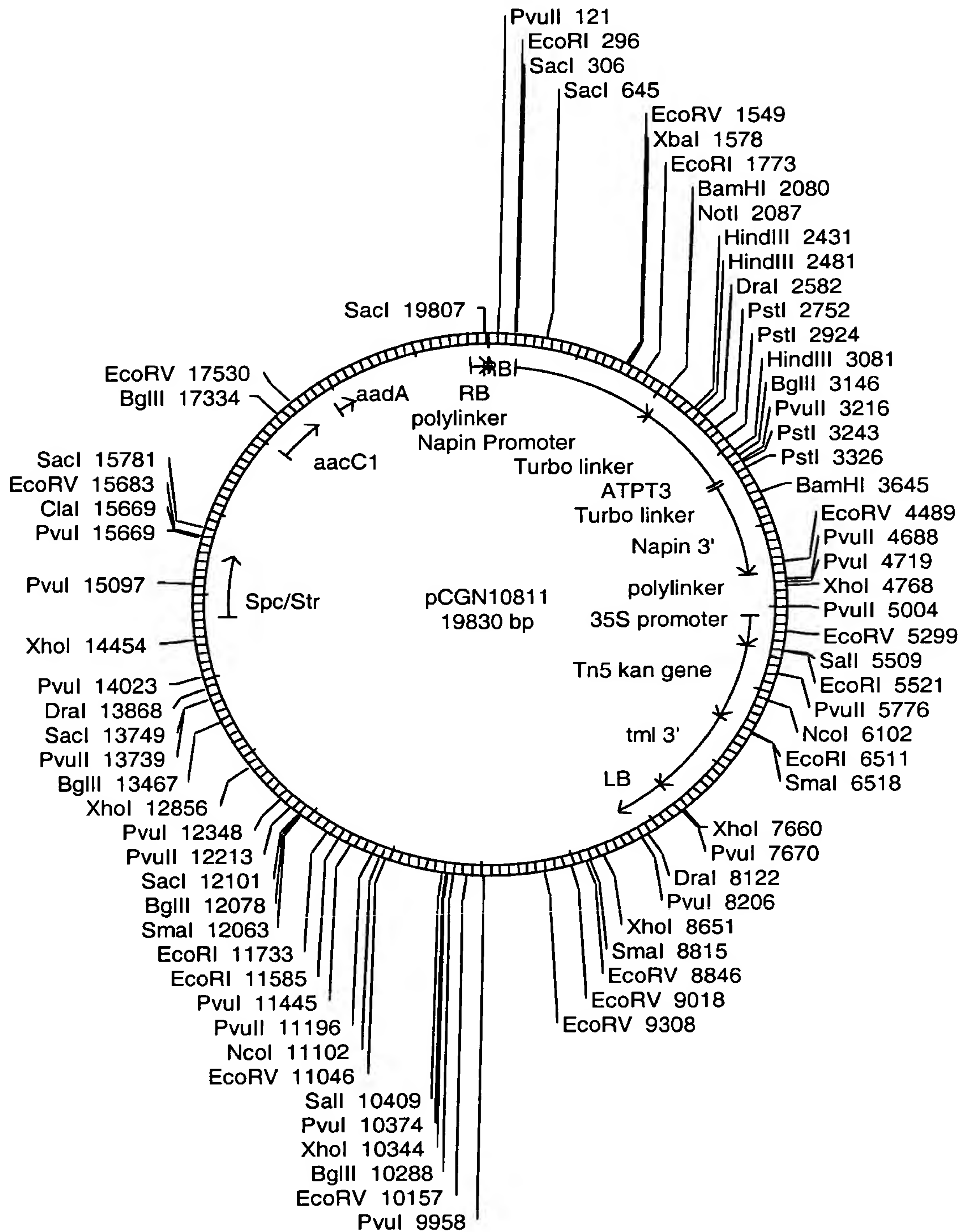


Figure 10

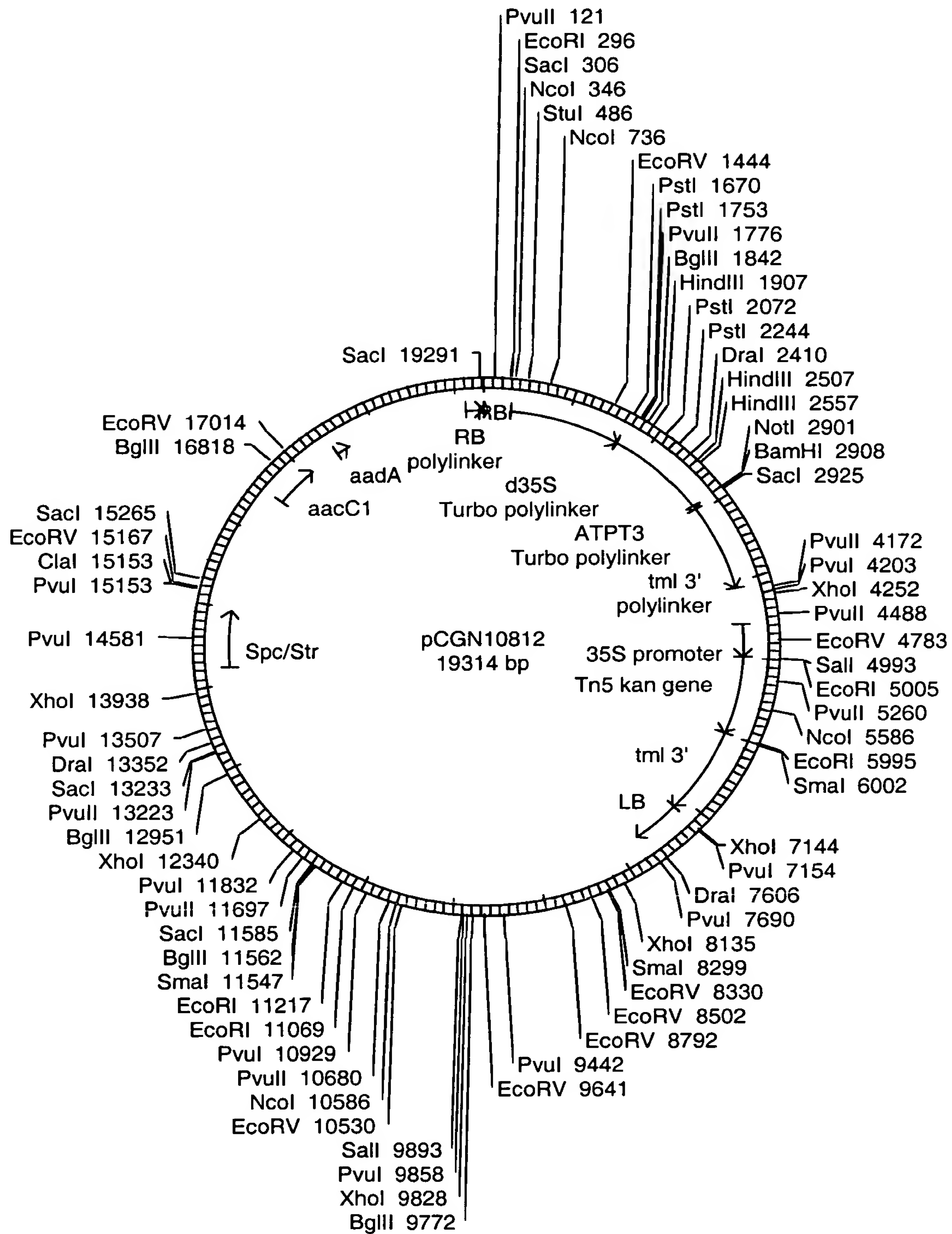


Figure 11

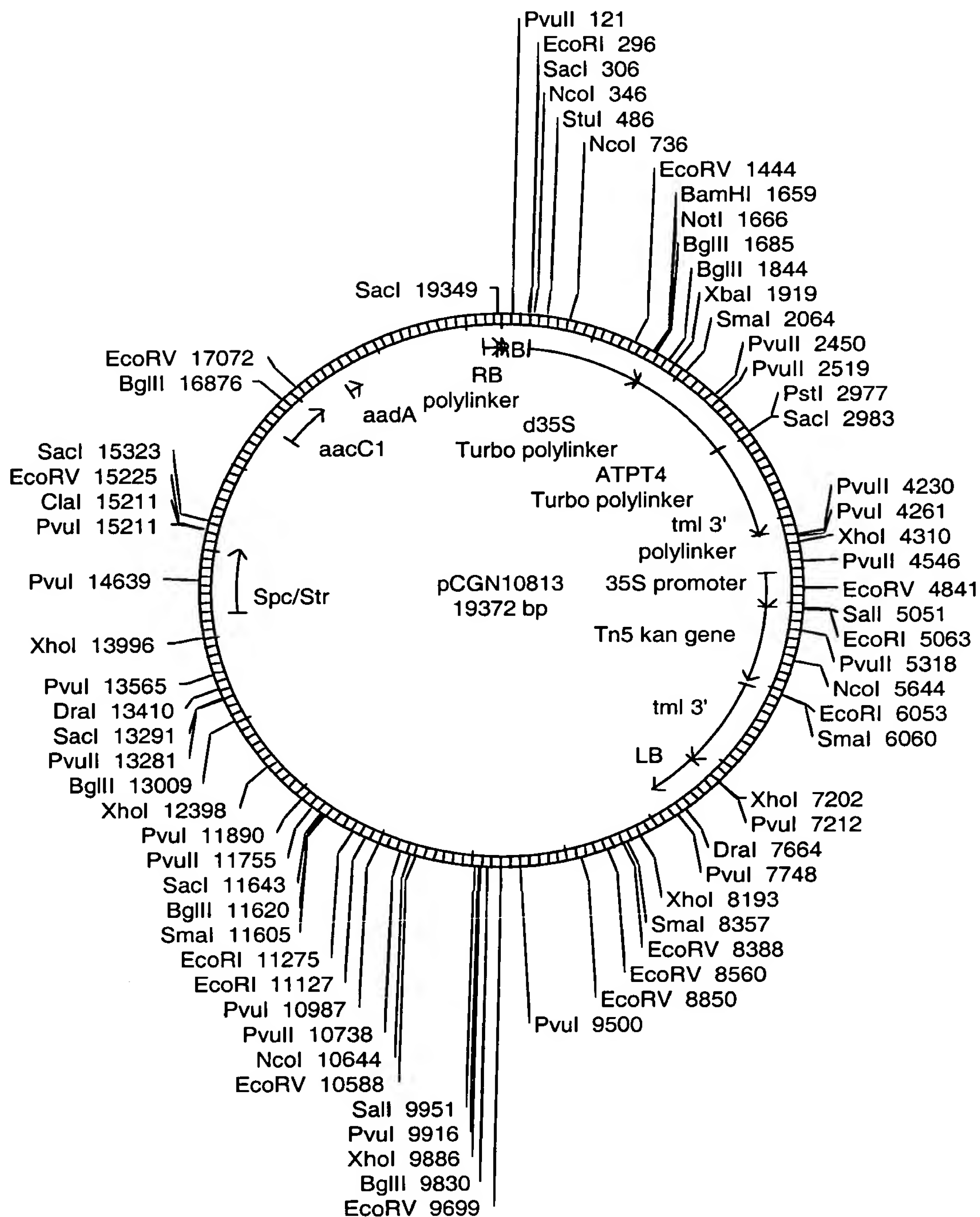


Figure 12

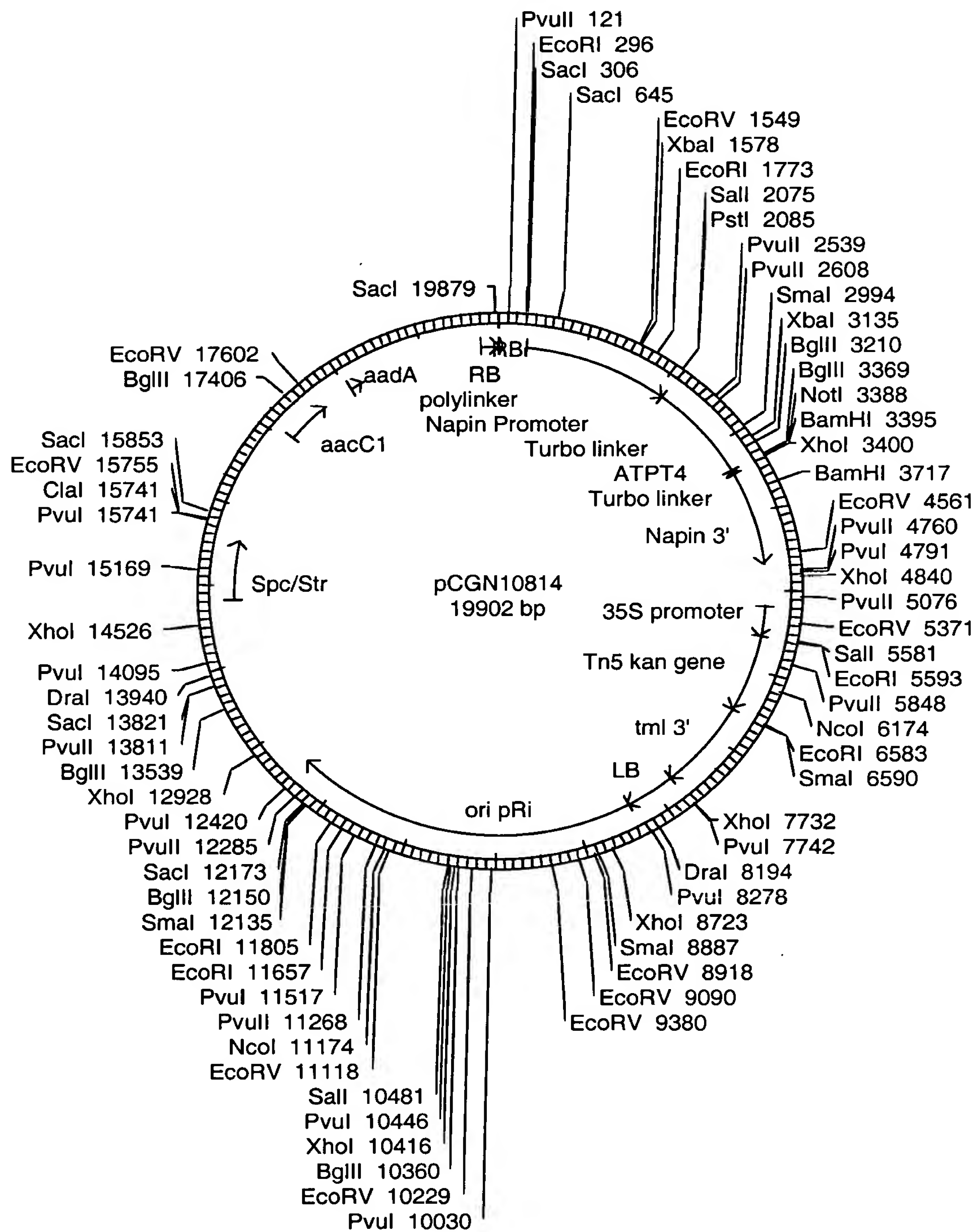


Figure 13

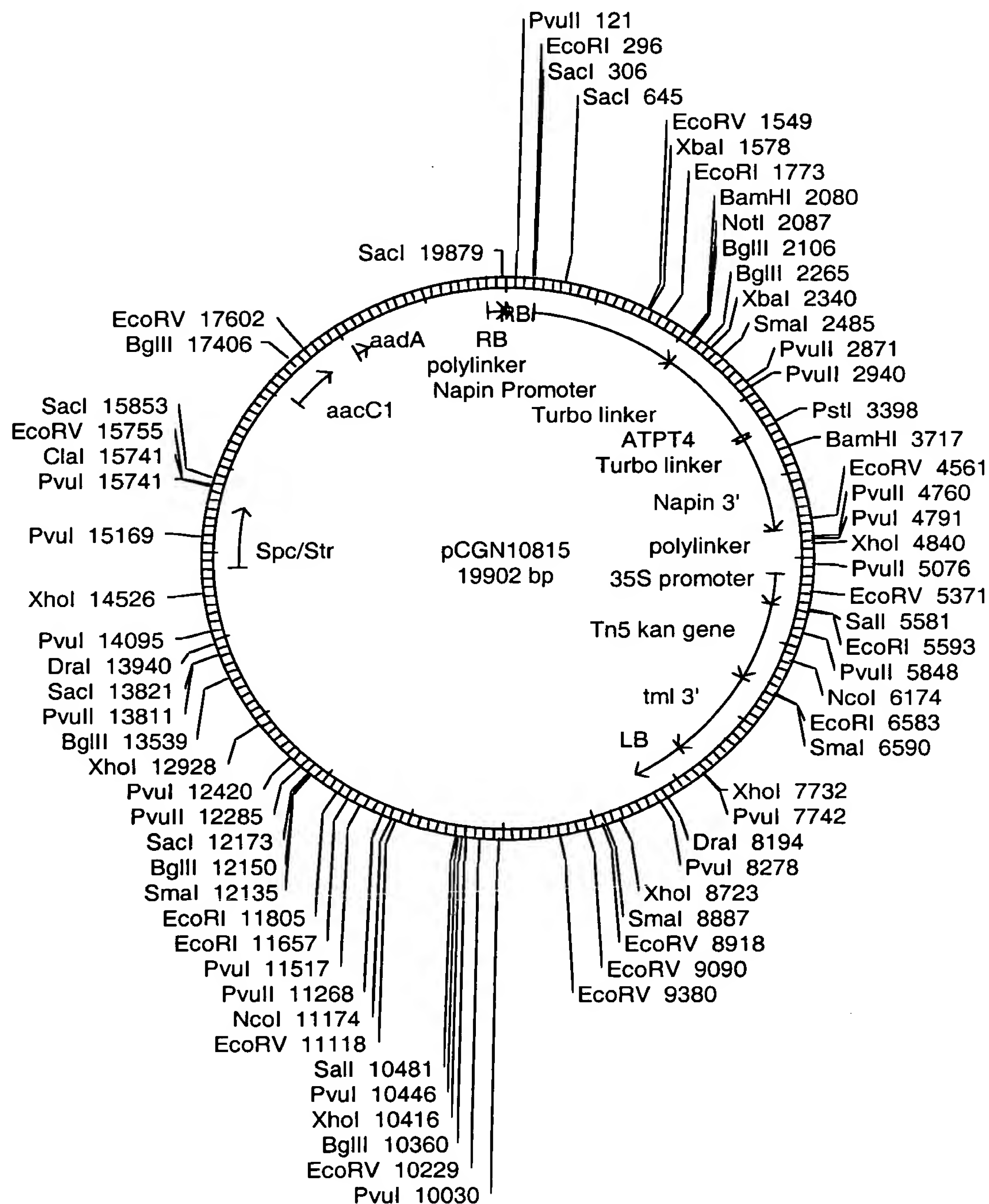


Figure 14

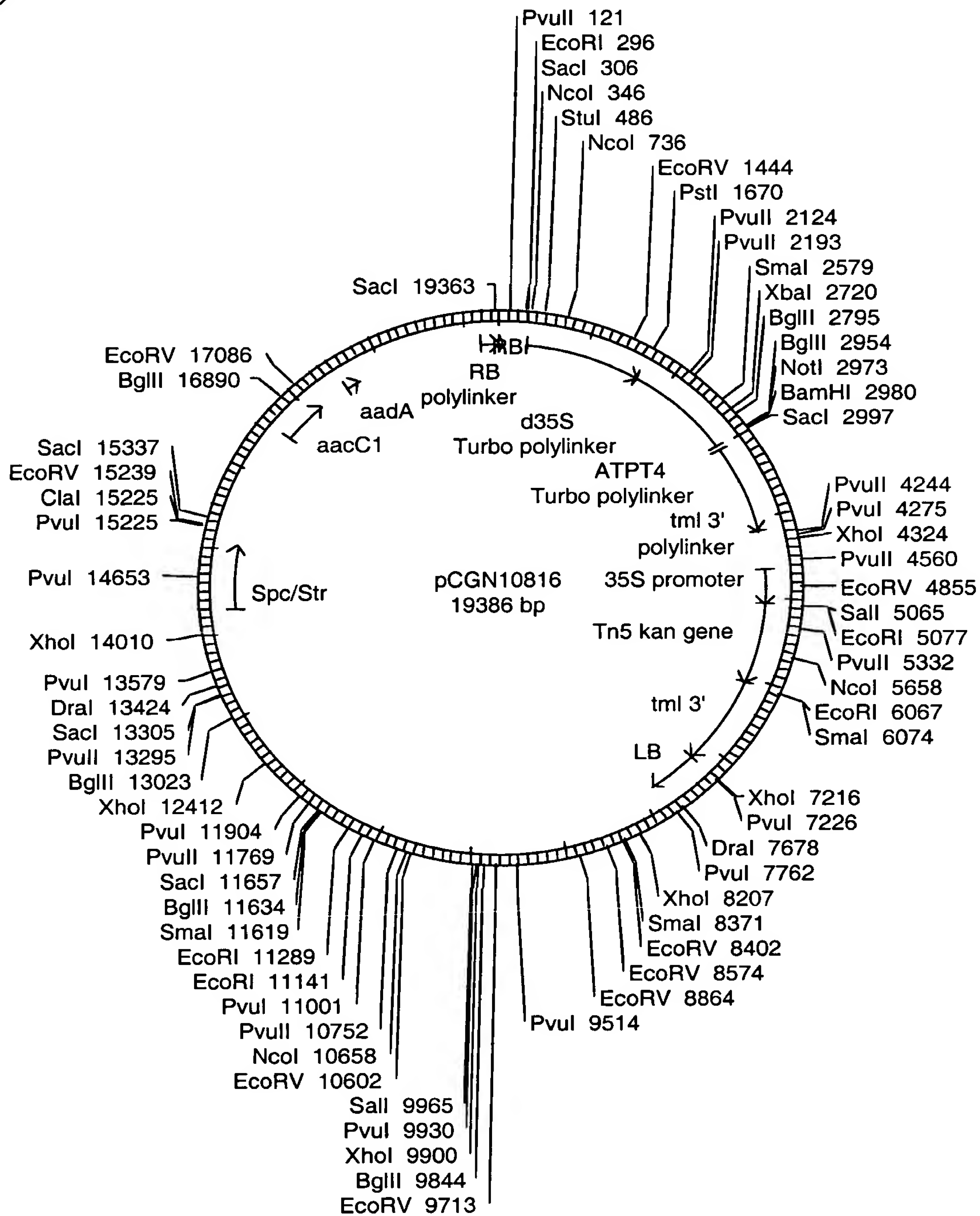


Figure 15

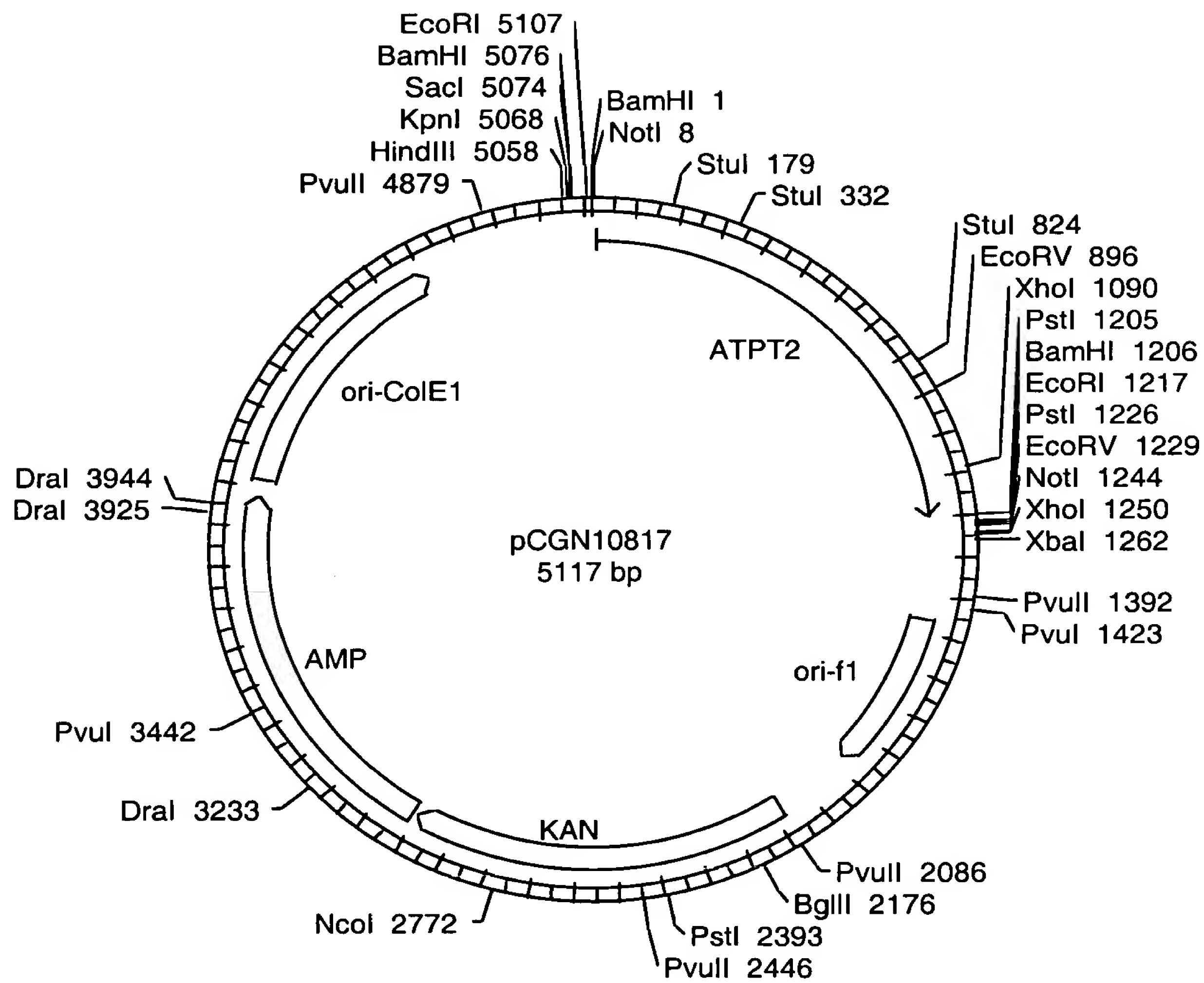


Figure 16

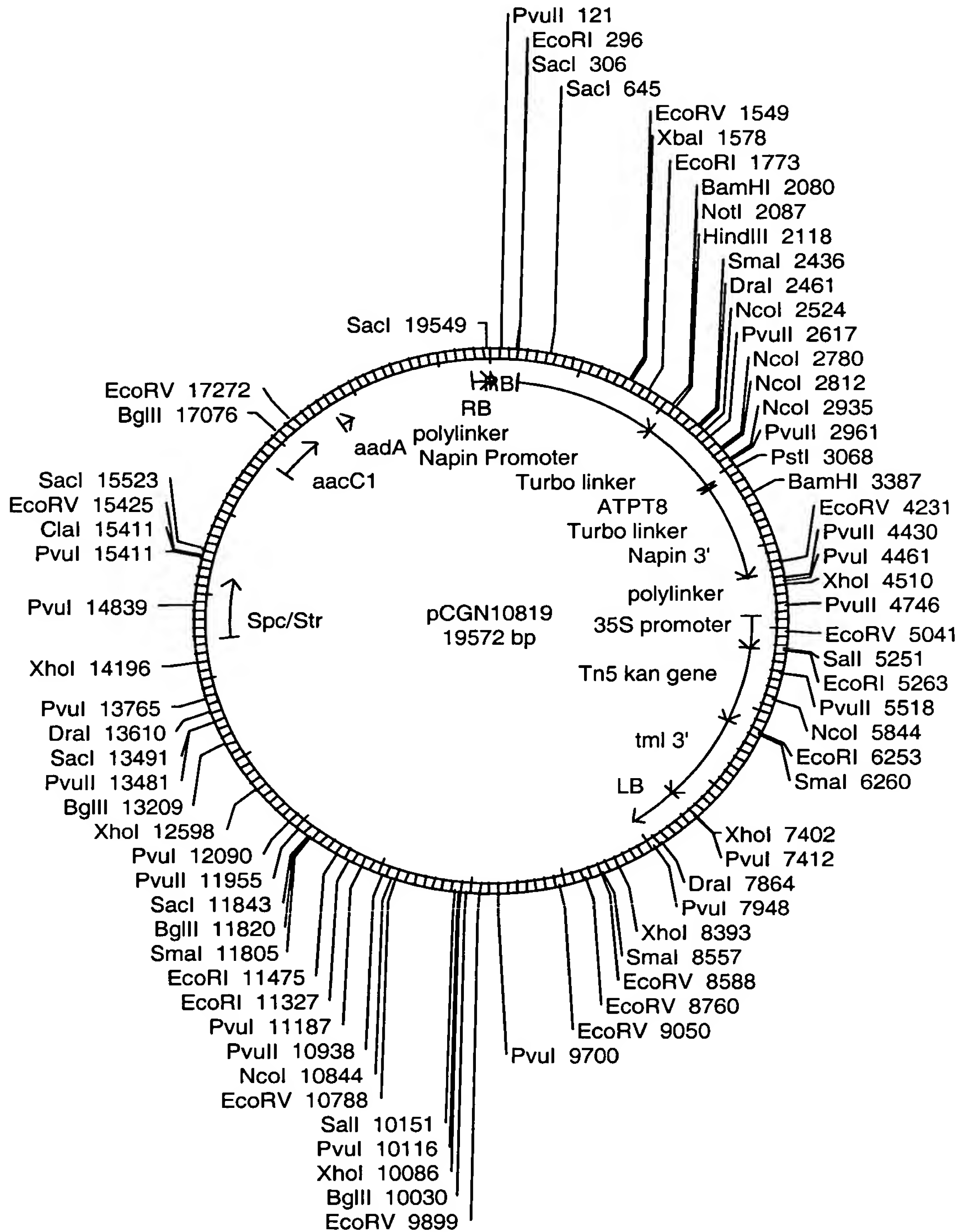


Figure 17

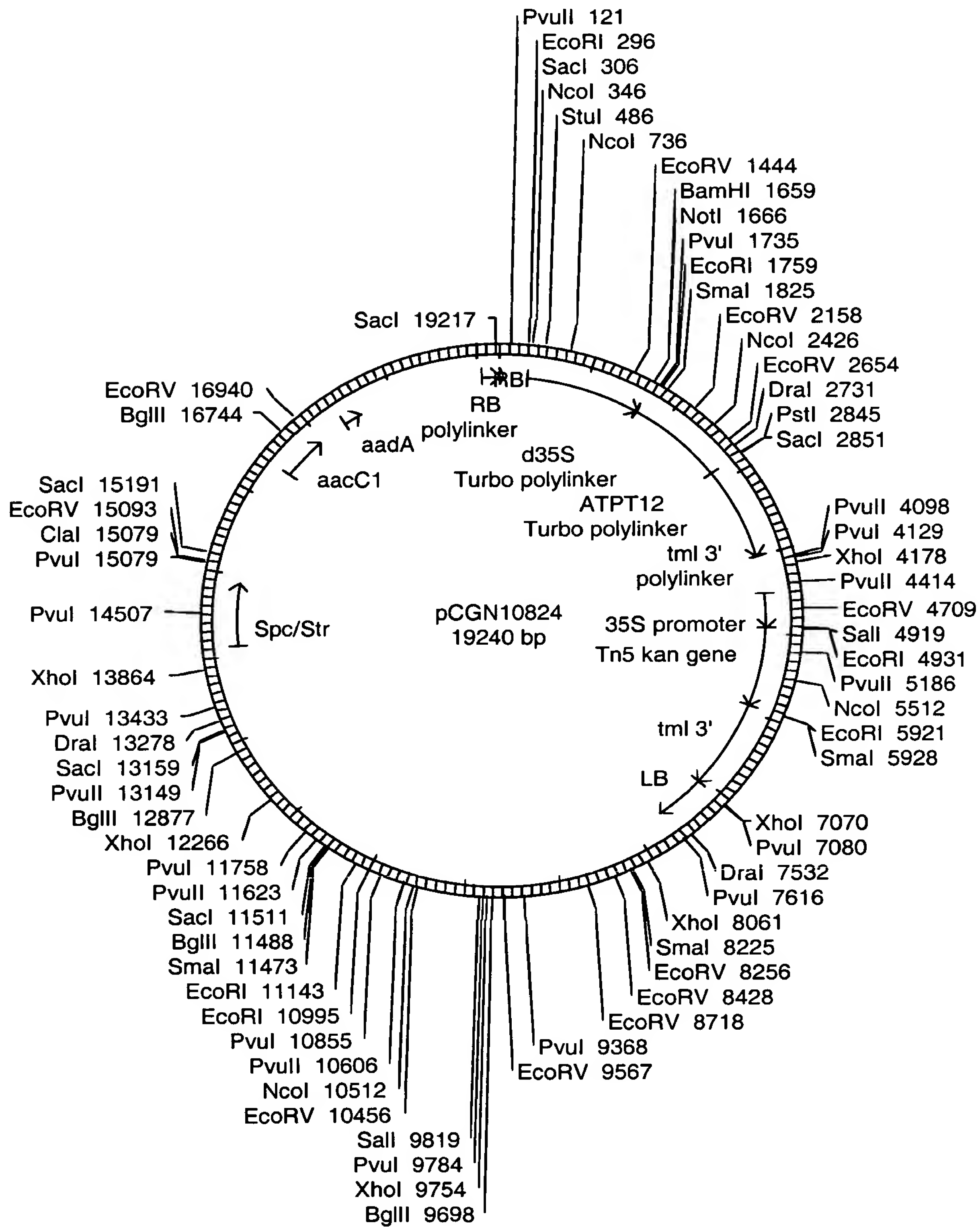


Figure 18

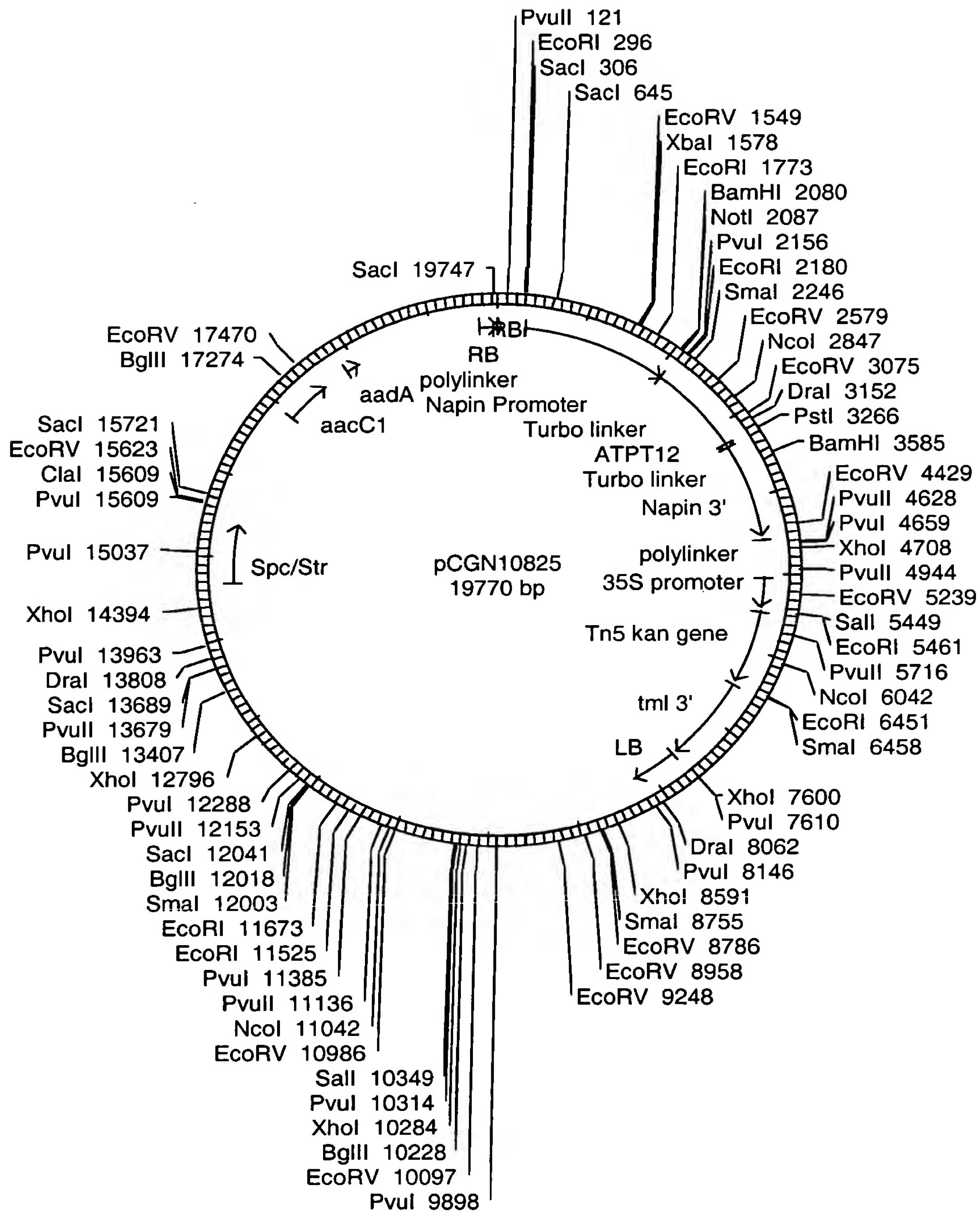


Figure 19

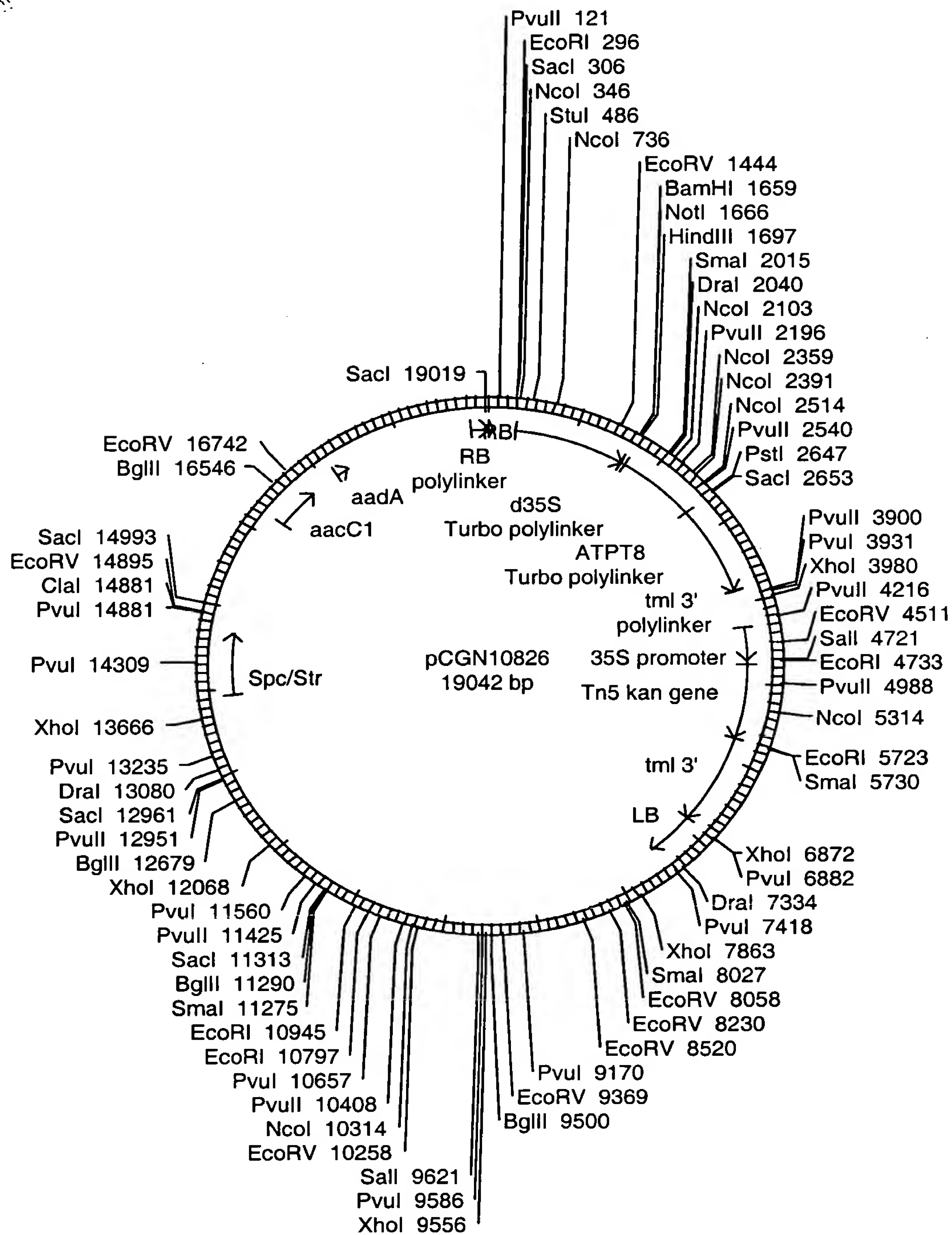


Figure 20

SLR1736 : MATIQAFWR : ---FSRPHITIGTTLS : ---VWAVYLLTILGD : ---G-NSNNSPAS : ---DDLVFGAWLACLLGNVYIVGL : 64
 SLR0926 : MVAQTPSS : ---PPLWLTIYLRWHKP : ---AGRLIIMIPALWA : ---VCLAAQGLPP : ---LPLIGTIALGTTATSGLCVV : 68
 SLL1899 : MVTGKIHRQDSMGAVCKSYQLTKP : ---RTIPELLITTAAS : ---MWIASEGRVD : ---LPKILLITLGGTAAASAQTL : 71
 SLR0056 : MSDIQNTGQ : ---NQAKARQLLGKGAAPGESSINKIRLQIMKPIITWIPLIWGVVCGAASSGGYIWSVEDFLKAITCMELSGPLMTGYTQTL : 88
 SLR1518 : MTESSPLAP : ---STAPATRKLWLAAIKP : ---PMTYTAVAVPTITVGSAAVAYGLTQWH : ---GDVFTIFILSATAIIAWINLS : 71
 M
 N 5D Did
 SLR1736 : NQIWDVDLDRINKPNLPANGDFSIAQGRWIWVGCQGVASLAIAWGLGLMGLTVGIS : ---LIIGTAYSVPVRLKRFSLLAALCLITVRGL : 152
 SLR0926 : NDLWDRDIDPOVERTKQRELAARAL-SVQVGHGVALVA-LICAGLAFLYLTPLS : ---FWLCVAAAPNTVAYPGAKRVFPVQLVL-SIL : 150
 SLL1899 : NCLFYDQDIDYEMLRTRARP IPAGKV-QPRHALIFALALGVLSFALLATFNVLSCG : ---LALSIGIVFMYLWYTHWLRKHTAQNIVIG-GA : 156
 SLR0056 : NDFYDRDIDDAINEPYRPIESGAISVPQVVTQILJLLEVAGIGVAYGLDVWAQHDFFPIMMVLTLCGAFVAYIYSAPPLKLKQNGWLGNY-AM : 177
 SLR1518 : NDVFDSDTGIDVRKAHSMVNLGTGNRLVFLISNFFLLAGVEGLMSMSWRAQDWI : ---VLELIGVAFLEGYTYQGPPFRLLGYLGLGELIC : 157
 N 5D Did
 SLR1736 : VVNLGLFETFERIGLGYPPITLTPHWLTLFTLVFTVAIAIFKDVDPDMEGDRQFKIQITLTIQIGKONMFRGTLLTLTG-CYLAMATWGLWA : 241
 SLR0926 : AWGEAVLISMS : ---AVTGDLETDATWLVWGATVFTLGFDTVYAMADREDDRRIGVNSSALFFG-QYVGEAVGFFFA-LTIGCLFYELGMI : 234
 SLL1899 : AGSIPPIVCGWA : ---AVTGDLSWTPPWVTFALIFLWTPPHFWALAMIKDDYAQVNVPMIPVIAGEEKTVSQIWIYYS : ---LVVVPFSLLEVYP : 241
 SLR0056 : GASVIALPWAG-HALFGLTENPTIMVLTIIYSLAGLGIAVNDFKSVGDRQLGKSLPVMFG-IGTAAWICVIMH : ---DVFAQAGIAGYLI : 263
 SLR1518 : LITEGPIAIAAAYYSQSQSFSWNLLTPSVFVGISTAILFCSHFHQVEDDLAAGKKSPIVRIG-TKLGSOVLTSVSVSYLITAGVLECH : 246
 L
 SLR1736 : AMPLNTARLIVSHLCLLALHWRSRDVHLESKTEIASFYQFIWKLEFLEYLLYPDALWLPNFSNTIF : --- : 308
 SLR0926 : LMLNPLYWLSLAIATVGVVIOYIQLSAPTEPKLYGQ-IEFGQNVIIIGFVLLACMLLGWI : --- : 292
 SLL1899 : LHQLGILYLAIAHLEGGQFLVKAWQLKQAPGDRDLARG-LEKFSIFLYMLCLANVIDSPVTHQLVAQMGTLLG : 316
 SLR0056 : YVHQQTYATIVLLLELPQITFQDMYFLRNPLENDVKYQ-ASAQPFLVFGMLATGLAIGHAGI : --- : 324
 SLR1518 : QAPWQTLLLIHAASLPWAVQLIRHVGVQYHDQPEQVSNCKFLAVNLHFFESGMLMAAGYGWAG : --- : 307
 P
 N 5D Did

Figure 21



Title: Nucleic Acid Sequences to Proteins Involved in Tocopherol Synthesis

Inventor: Subramaniam et al.

Atty Docket: MONS:038US

Sheet 22 of 40

Replacement Sheet

```
ATPT2 : -----MESLLSSSLVSAAGGFCWKKQNLKHLSEIRVLRCDSSKVAKPKFRNNLVRPDGQSSLLLPKHKSFRVNATAGQ : 80
SLR1736 : -----
ATPT3 : MAFFGLSRVRRLLKSSVSTPSSSSALLQSQHKSLSNPVTTHYTNPTKCYPSWNDNYQVWSKGRELHQEKFFGVGWNRYRLICGMSSS : 89
SLR0926 : -----
ATPT4 : -----MWRRSVVYRFSRISVSSSLPNRPLIPWSRELCAVNSFSQP-----PVSTESTAKLGITGVRSDANRVFATA : 67
SLL1899 : -----
ATPT12 : -----MTSILNTVSTIHSSRVTSVDRVGVLRLNSDSVEFT-----RRRSGFSTLIYESPGRRFVVRAAETDT : 63
SLR0056 : -----
ATPT8 : -----
SLR1518 : -----MTES : 4
```

```
ATPT2 : PEAFDSNSKQK-----SFRDSDAFYR-----FSRPHVTGTVLSILS-----VSFLAVEKVS--DISPLFTGKLE : 140
SLR1736 : -----MATHQAFWR-----FSRPHVTGTVLSVWAVY-----LLTILGDN-SVNSPASDLVFG : 49
ATPT3 : SSVLEGPKKDDKEKSDGVVVKASWIDLYLPEEVGYAKLARLDKPIGTWLLAWPCWMS-----IALAADPGS--LPSFKYMAFGC : 170
SLR0926 : --MVAQTPSSP-----PLWLTIIYL-----LRWHKPAGRILMIPALWA-----VCLAAQ--G--LPPLPLIGTIAL : 56
ATPT4 : TAAATATATTG-----EISSRVAALAGLGHYAR-----CYWELSKAKLSMLVVATSG-----TGYILGTGNAAISFPGLCYTCAG : 138
SLL1899 : TKIHRQHDSMG-----AVCKSYQLTKP-----RIIPLLTITTAASMWI-----ASEGR--VDLPKLEITLLG : 60
ATPT12 : DKVKSQTPDKAP--AGGSSINQLLGKAS-----QETNWKIRIQLTTPVTPPLVWGVVCGAASGNFHWTPEDVAKSHLC : 139
SLR0056 : QNT-GQNQAKA-----RQLGKMGKGAAP-----GESSIWKIRIQLMKPITWIPLIWGVVCGAASSGGYIWSVEDFEKALTC : 73
ATPT8 : EVPKLASAAEY-----FFKRGVQKQF-----RSTILLMAATALNMRVP-----EALIGEST--DIVTSELRVRQR : 63
SLR1518 : SPLAPSTAPAT-----RKLWLAAIKP-----PMTVAVVPITVG-----SAVAAYGLTG--QWHGDMFTIFLL : 59
```

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ATPT2 : AVVAALMNIYIVGENQDSEVEIDKVNKPYPPLASGEYSVNTGIAIVASFSMSFWLGIWVGSWPLFWALFVSFMLGTAYS-INIPILR : 228
SLR1736 : AWLACLLGNVYIVGLENQLDVDEIDRINKPNLPLANGDFSTIAQGRWIVGLCGVASIAIAWGLG-LWLGLTVGISLIIGTAY--SMPVVR : 134
ATPT3 : GALL--TRGAGCTINDLLDQPIDTKVDRTKLRPIASGLTTPFQGTGFLGQLLGLG-----ILLQNNYSRVLGAS--SLLIVF : 246
SLR0926 : GTLA--TSGLGCVNDLWDRDIDPQVERTKQRLAARALS-VQVGIQVAVLALCAAG-----LAFYLTPLSFWLCVA--AMPVIV : 132
ATPT4 : TMMI--AASANSNQLFEISNDPKMKRTMLRPLPSGRISVPHAVAWATHAGASGACL-----LASKTNMLAAGLASAN--LVLYAF : 215
SLL1899 : GTLA--AASAQTLNCTIDQDIDYEMLRTRARPPIPAKQVQPRHALTFALAGVLSFAL-----LATFVNVLSCCLALSG--IVFYML : 137
ATPT12 : MMSGPGCTTGYTQTINDWDRDIDDAINEPYRPIPSGAISEPEVITQMVVLGLGIGILD-VWAGHTTPTVLYALG--GSLISY : 223
SLR0056 : MLLSGPLMTGYTQTLNDFDRDIDDAINEPYRPIPSGAISVPQVVQTLILVAGIGVAYGLD-VWAGHDFPMMVLTG--GAFVAY : 157
ATPT8 : GIAE--TEMIHVASLLHDDVLDADTRRGVGSNLVVMGNKMSVAGDFLLSRACGAL-----AALKNTEVVALLATAVEHLVTGETM : 144
SLR1518 : SATLA--IAWINLSNDVFDSDTGIDVRKAHSVVNLTGNRNVLVFLISNFFLLAGVGLGMSMS--WRAQDWTVLELIGVA--FFIGY : 138
```

n d d

Figure 22A



ATPT2 : WKR-FALVAAMCILAARAIIVQIAFYTH-IQTHVFGRPILFTRPLIFATAFMSFFSVVIAIFKDIPIEDKI-FGHSFSVTLC-QKR : 313
SLR1736 : LKR-FSLLAALCILTVRGIVNGLFLEF-FRIGLGYPTLITPIMV-LTLFILVFIVVAIAIFKDVDPDMEGDRQ-FKHQITLTIQIG-KQN : 218
ATPT3 : SYP-LMKRFTFWPQAFGLTUNWGALEGG-WT-AVKGSIAPIAVLPEYLSGVCVTLVYDTIYAHQDKEDVK-VGVKSTALRFG-DNT : 328
SLR0926 : AMP-GAKRVFPVPQLVLSIAWGAFLIS--WS-AVTGDLIDATWV-LWGATVFWTLGFDTVYAMADREDDRR-LGVNSSALFFG-QYV : 213
ATPT4 : VMT-PLKQLHPINTWVGAVVGAIPPLIG-WA-AASQIISYNSMI-LPAALYFWQIPHFMALAHLCRNDYAA-GGYKMSLFDPP--S : 294
SLR1899 : VYTHWLKRHTAQNIIVHIGGAAGSIPPLVG-WA-AVTGDLISWTPWV-LFALIFLWTPPHFWALALMIKDDYAA-VNVPMLPVIAGEEKT : 220
ATPT12 : IYS-APPLKQKQNGWVGNFALGASYISLPWAGQALFGTLTPDVVW-LTLLYSIAGLGIATVNDFKSVEGDRA-LGLQSLPVAFG-TET : 308
SLR0056 : IYS-APPLKQKQNGWVGNFALGASYIALPWAGHALFGTLNPTIMV-LTLLIYSLAGLGIATVNDFKSVEGDRO-LGLKSLPVMFG-IGT : 242
ATPT8 : EITSSTEQRYSMDYYMKTYKTSLSNSCKAVAMLTGQAEVAVILAFEYGRNLGLAFQIIDDILDTGTSASLCKGSLSDIRH--GV : 231
SLR1518 : TYQGPFRGLGLGELICLITFGPLAI-AAAYYSQSQSFSWNLEIT-PSVVFVGISIAIILFCSHFHQVEDDLA-AGKKSPIVRLG-TKL : 223

ATPT2 : VFWTCVTLIQMAYAVAIIVGATSPFIWSKVISVWGHVILATTTIWARAKSVDSLSSKTEITS--CYMFIWKLFYAEYDELPLFLK----- : 393
SLR1736 : VFRGTILITGCVLAMAIVGWAAMPLNTAFINSHLCILALIWRRSRDVHLESKTEIAS--FYQFIWKLFYAEYDELPLFLK----- : 304
ATPT3 : KLWITGFGTASIGFALSFGSADLQWQYVASYIAAASQIIGWQIGTADLSSGADCS-----RKFFVSNKWFAGLIFSGVVLGRSFQ-- : 407
SLR0926 : GEAVGFFALTIGCFYLGMLMLNPLYWLSIAIAI--VGVNFIQYIQLSAPTPEP-KLY-----GQIFGQNMIIIGFVLEAGMLLGWL--- : 292
ATPT4 : GKRAAVALRNCFYMIPTGFIAYDWGLTSSWFCLESITLTLAIAATAFSRYDRDTHKA-----RKMFIHASLFLPVFMSGLLHRVSND : 379
SLR1899 : VSQHWYSLLVVPFSLLVYPLHQLGILYLALAIID--GGQFIIVKAWQLKQAPGDRDIA-----RGLKFSIFYLMELCLAMVDDSLPVT : 303
ATPT12 : AKWICVGAIDITQLSVAGYLIVASGKPYVALALVALI--IPQIVFQFYFLKDPVKYDVK-----YQASAQPFVLVLFHTALASQH--- : 387
SLR0056 : AAWICVIMIDVFQAGIAGYLIVYHQQLYATIVGLLE--IPQITFQDMYFLRNPLENDVK-----YQASAQPFVLVLFHTALASQH--- : 324
ATPT8 : ITAPIIFAMEEFPQIREVVDQVEKDPRNVDIAEYLGKSKGIQARELAMEHANLAAAIGSLPETDNEVMKRSRRALIDLTHRVITRN : 320
SLR1518 : GSQVLTLSVVSLSYLITAGVICHQAPWQTLTLIASIPWAVQLIRHVQYHQDQPEQVSNCK---FIAVNLHFFSGMLMAAGYGWAGLG-- : 307

ATPT2 : ----- :
SLR1736 : NTIF----- : 308
ATPT3 : ----- :
SLR0926 : ----- :
ATPT4 : NQQQLVEEAGLTNSVSGEVKTKRRKRVAPPPVAYASAAPFPLPAPSFYSP : 431
SLR1899 : --HQLVAQMGTLLLG----- : 316
ATPT12 : ----- :
SLR0056 : ----- :
ATPT8 : K----- : 321
SLR1518 : ----- :

Figure 22B

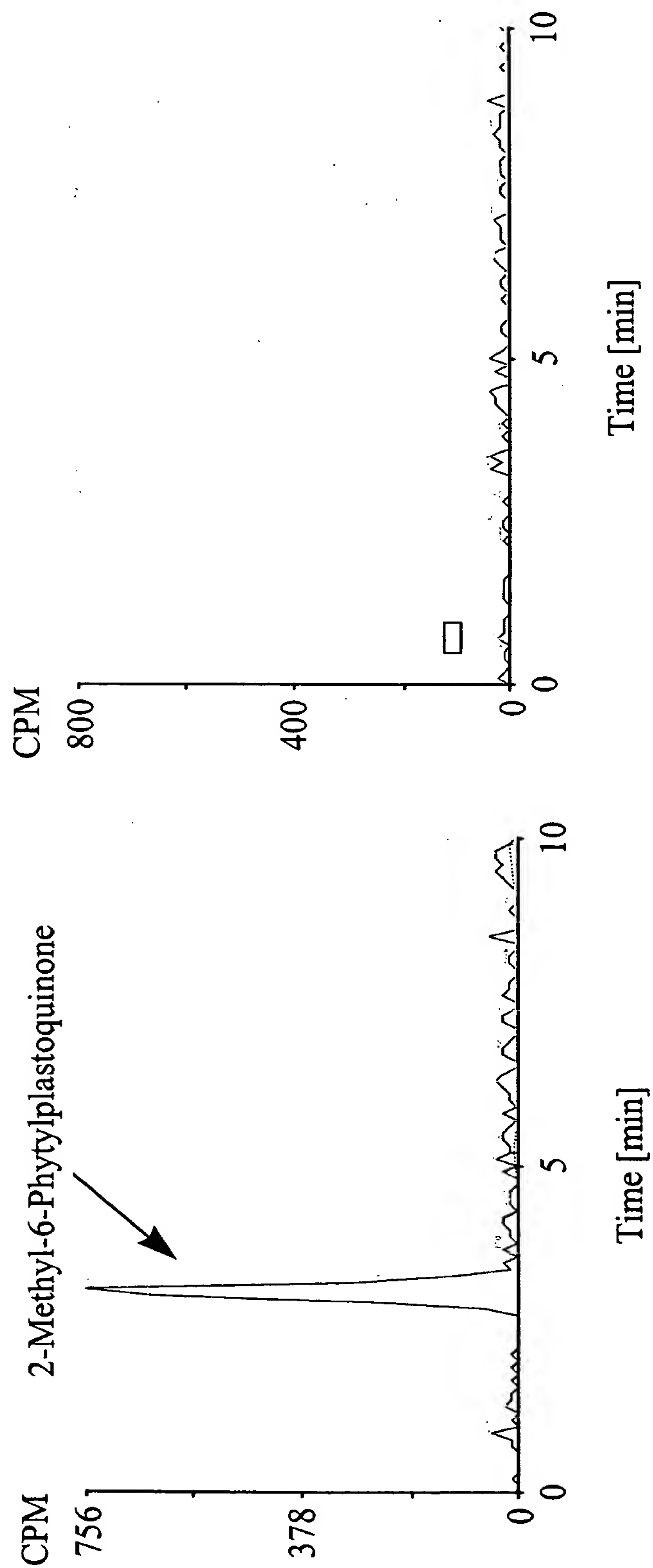


Figure 23

Synechocystis 6803 wild type *Synechocystis* slr1736 knockout

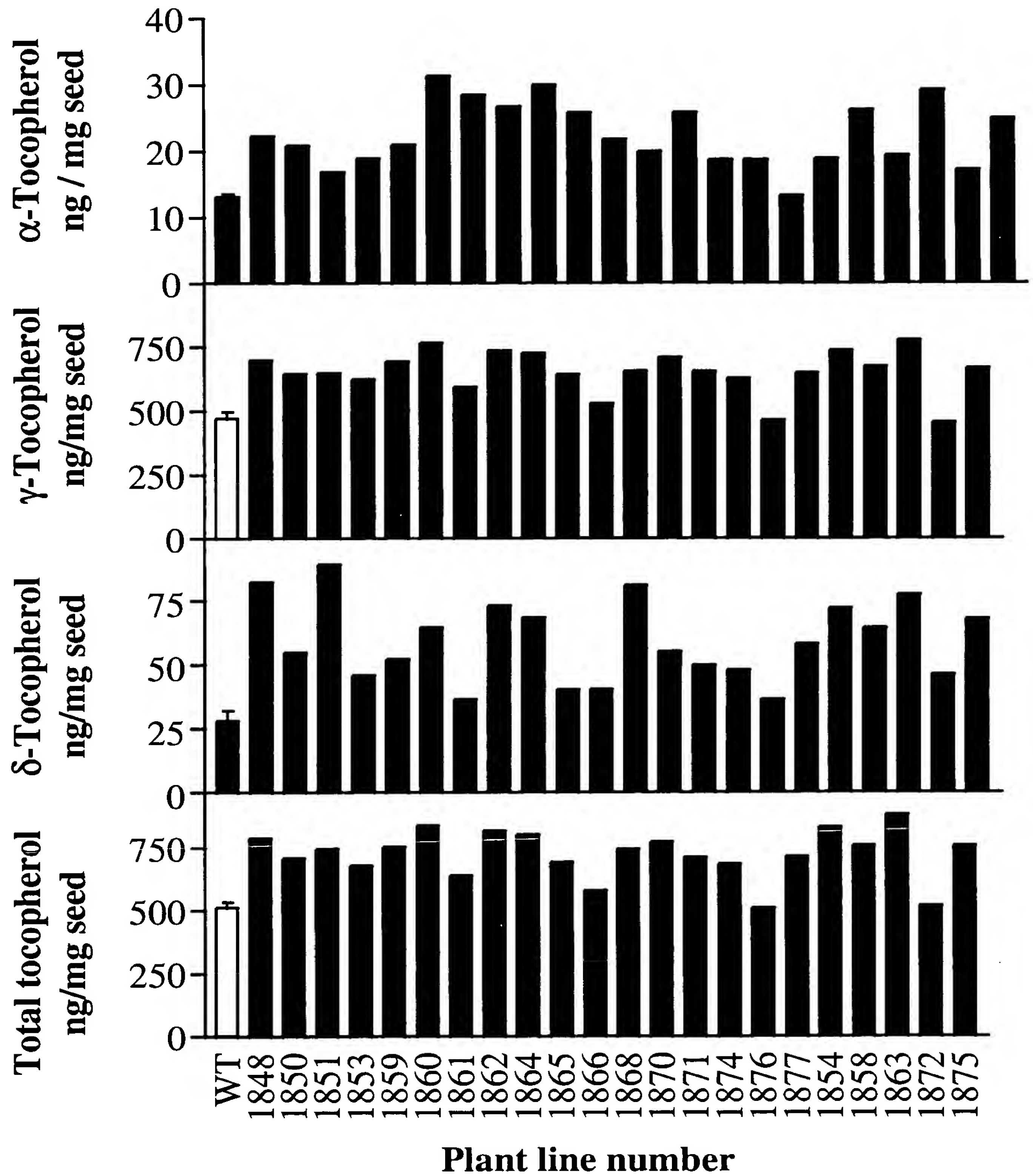


Figure 24

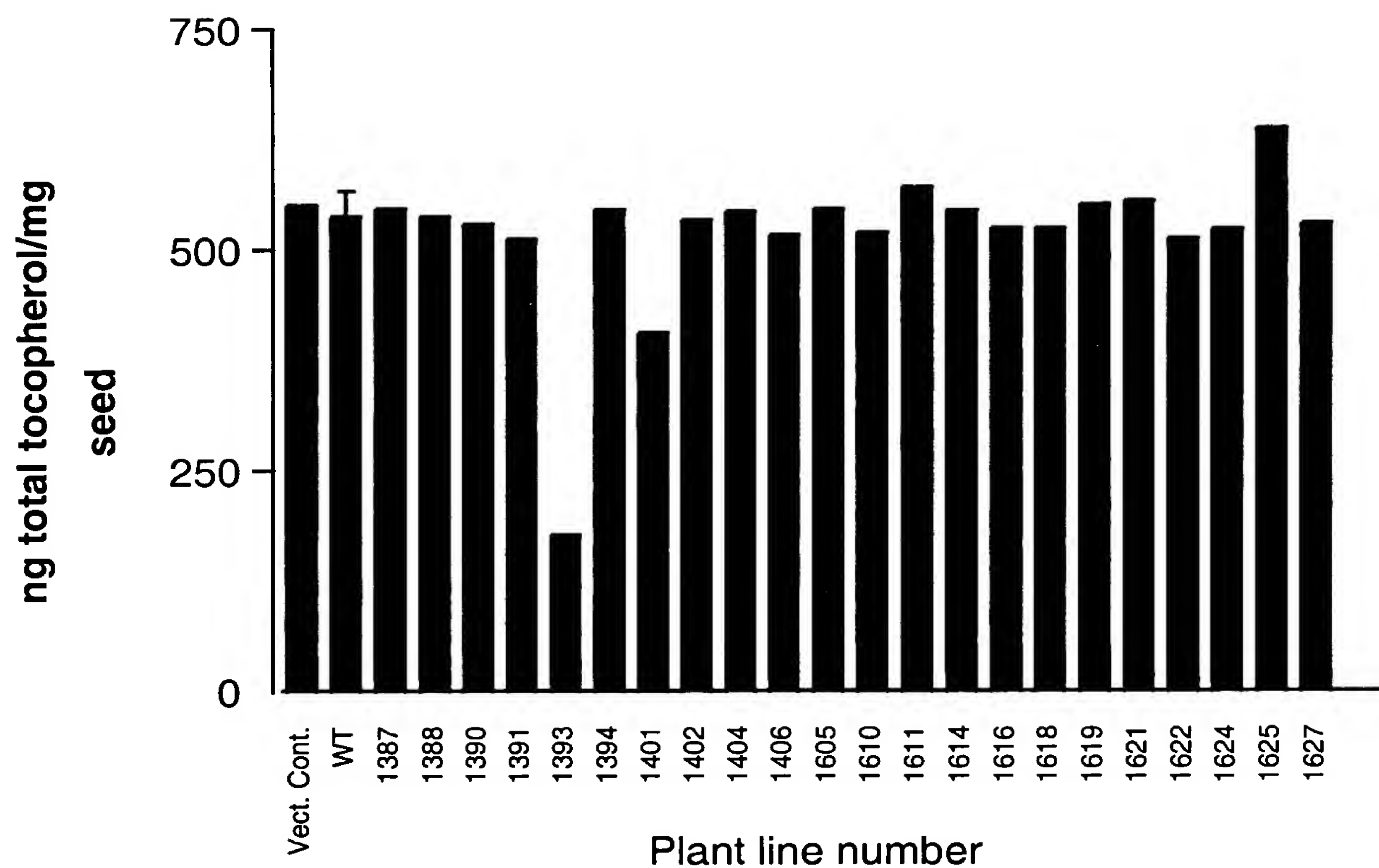


Figure 25

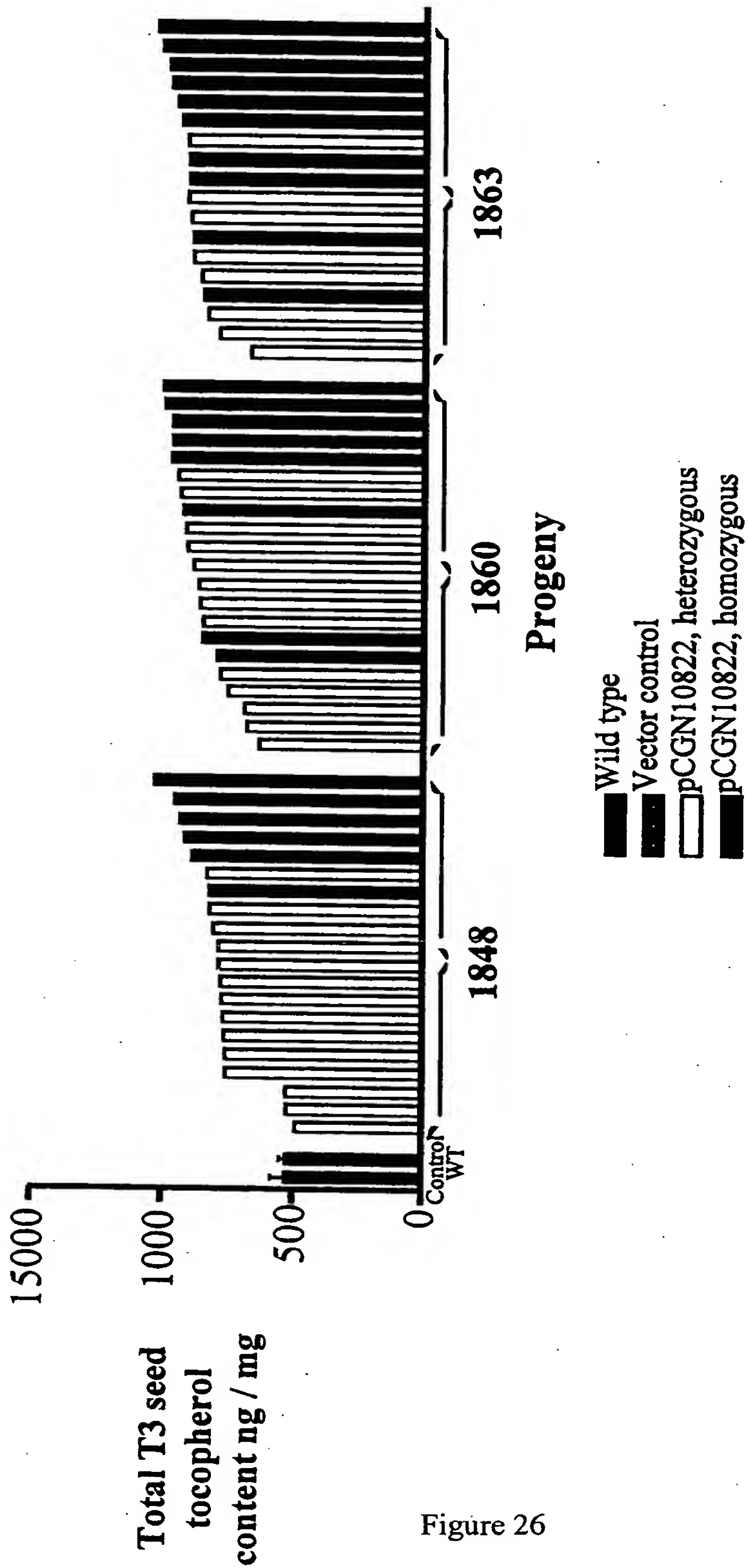


Figure 26

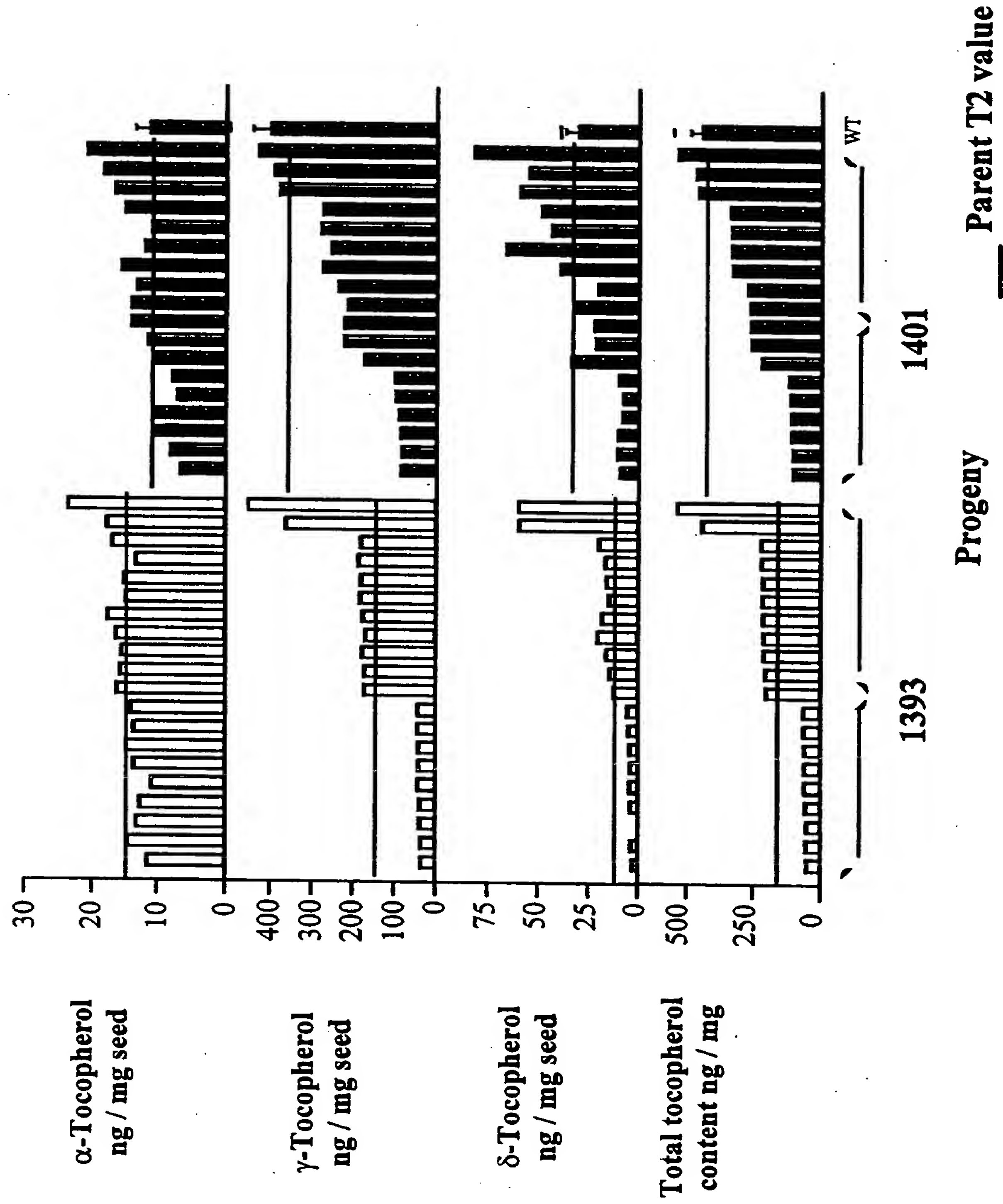


Figure 27



Total tocopherol in Napin ATPT2 Canola Seed

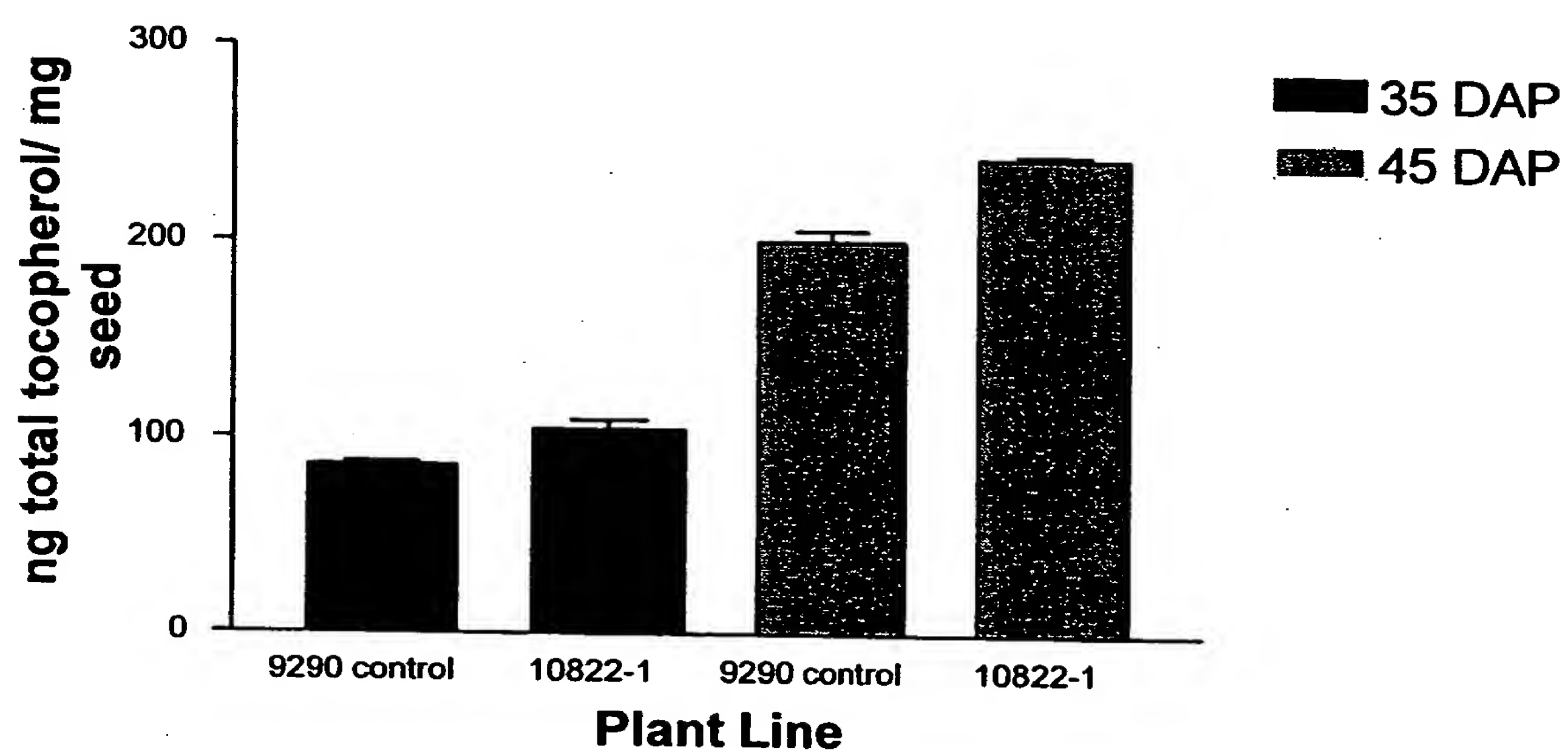


Figure 28

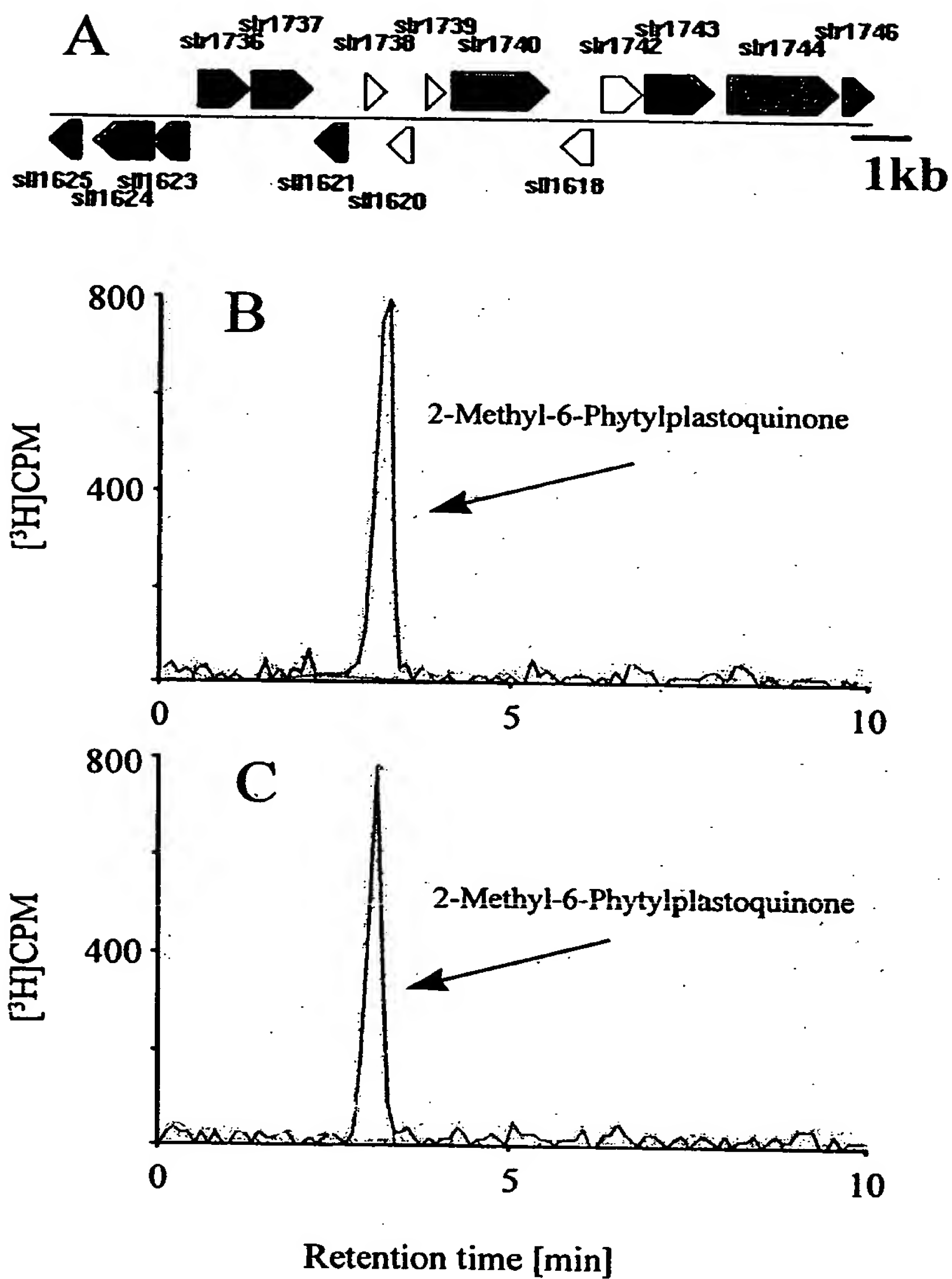
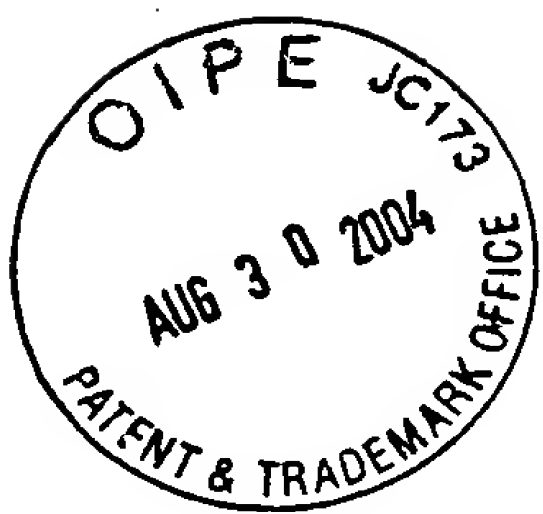


Figure 29

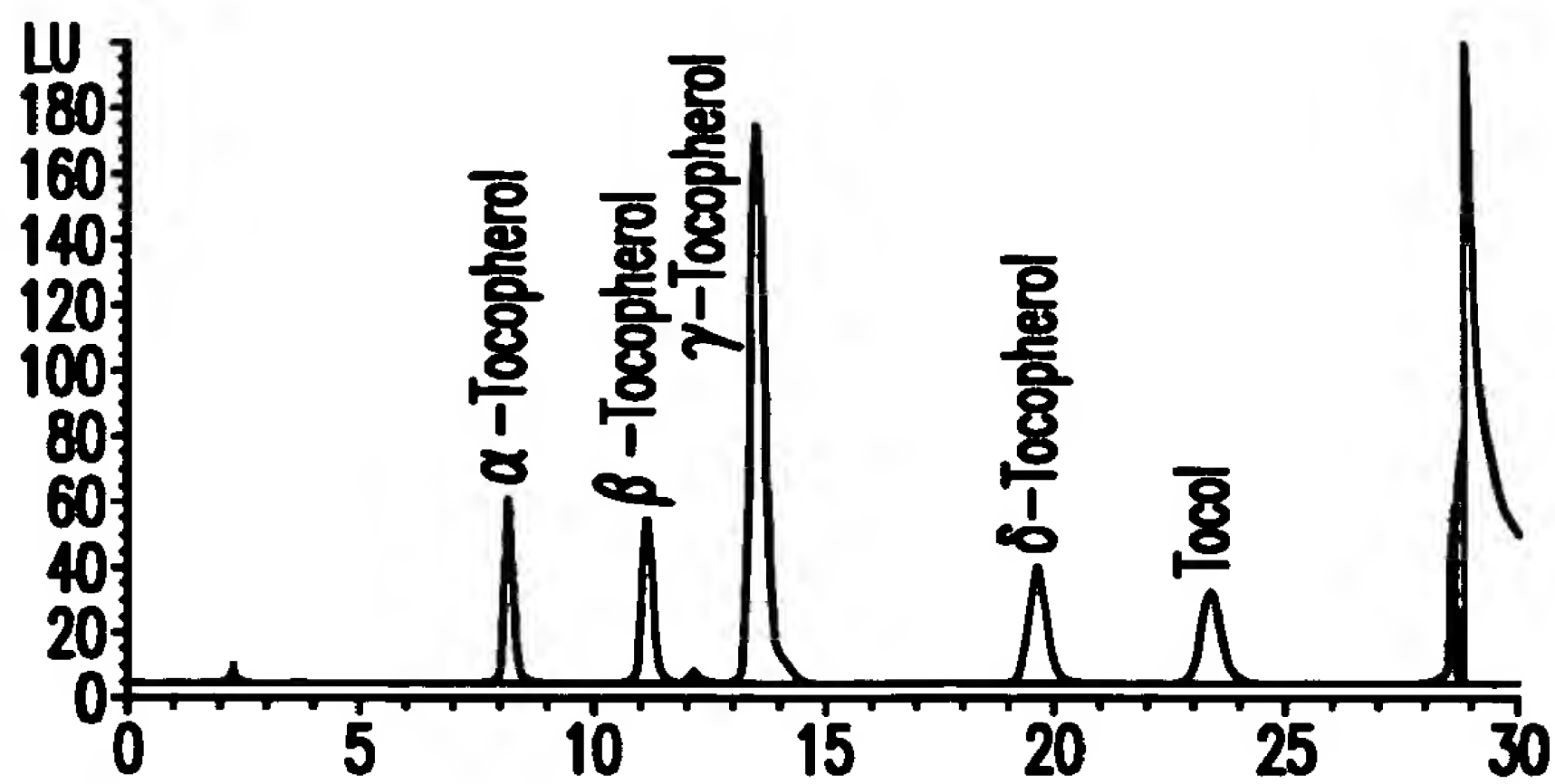
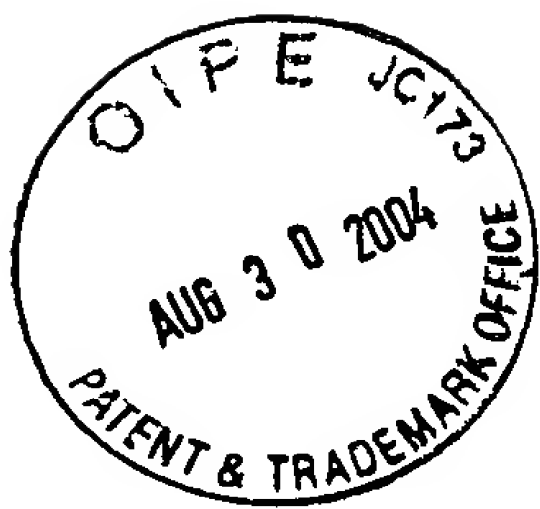


Figure 30A

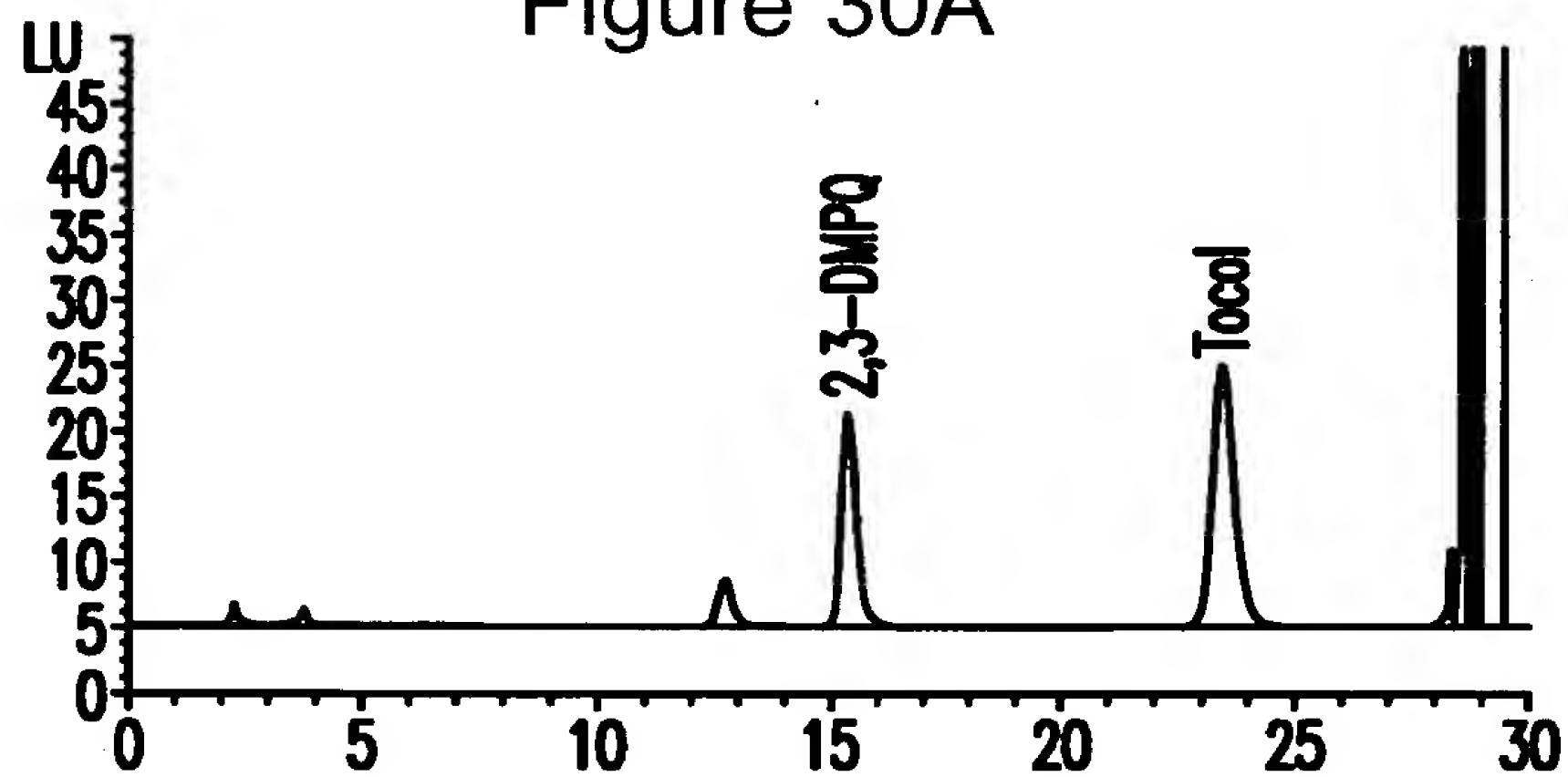


Figure 30B

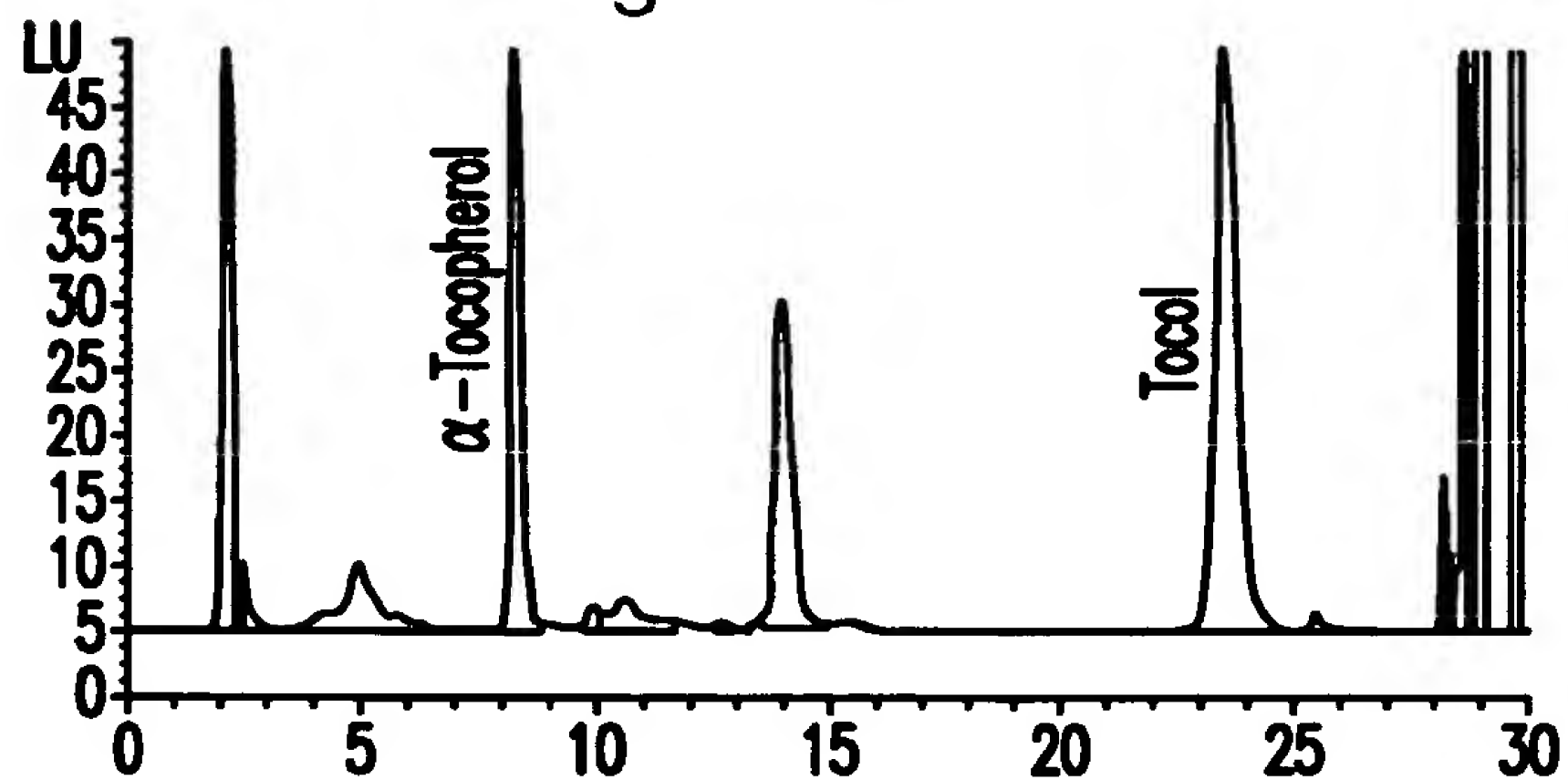


Figure 30C

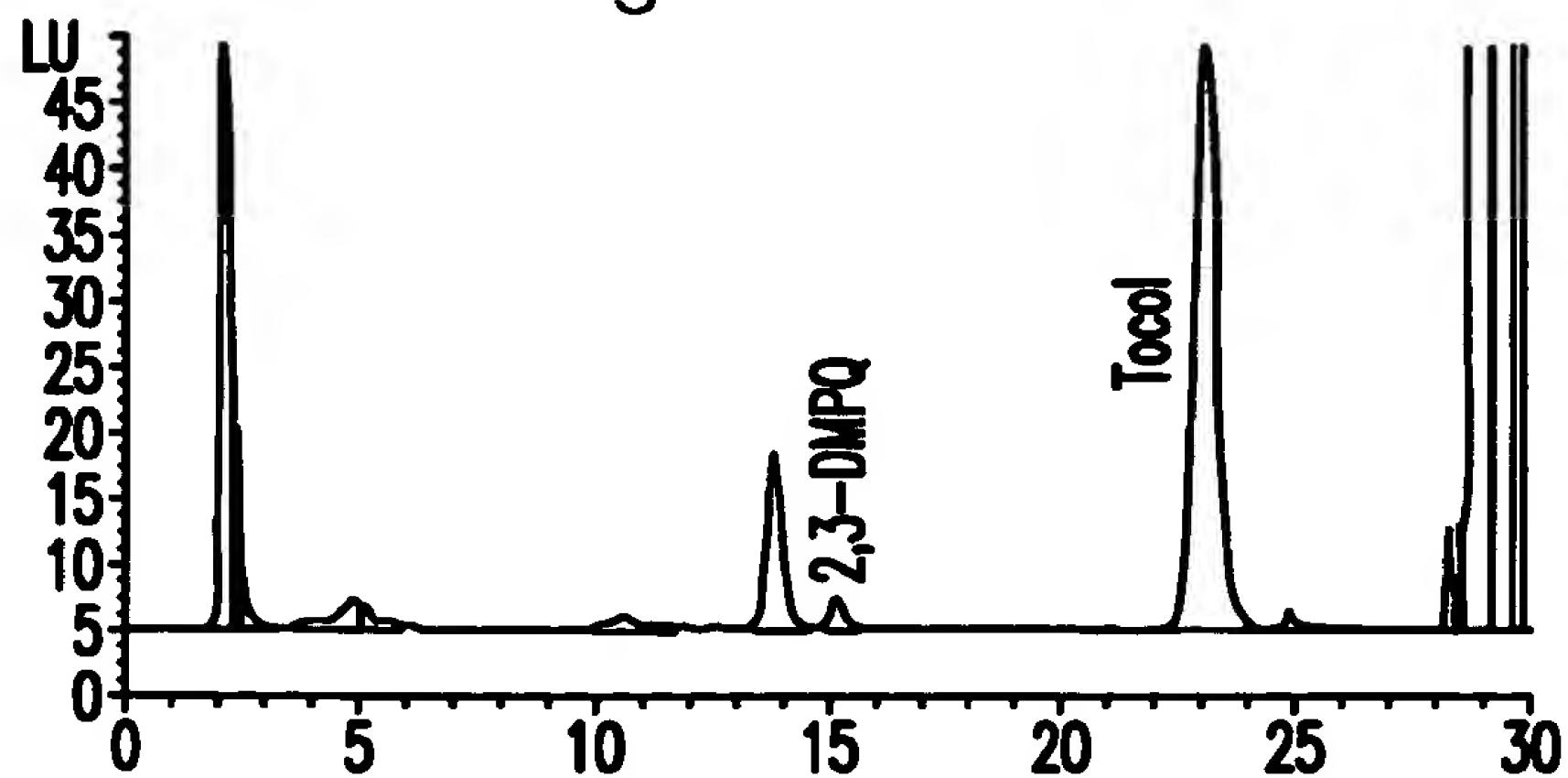
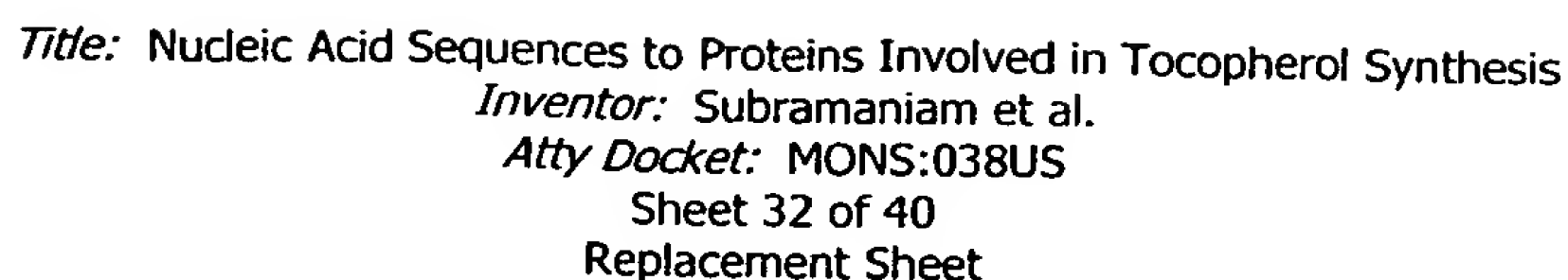


Figure 30D



```

Query-      12194 CACACGTTCTCGTCCTTTTCTTCTCCTCTCTGCATTCTTCACAGAGTTTGTCACCACCA
genomic
ATCEA4C371+    1 ----- C est
               :       :       :       :       :       :       :       :
Met
Query-      12134 ACACCAAACA CACAATTTCAGATTCTTTTCATATTTCCTCTCTCTCCATTATGGA
ATCEA4C371+    2 ACCCCAAACATCACAAATTTACATTCTTTTGCATATTCTTCTTCTTCCATTATGGA

Query-      12075 GATACGGAGCTTGATTGTTTCTATGAACCCTAATTTATCTTCCTTTGAGCTCTCTCGCCC
ATCEA4C371+    62 GATACGGAGCTTGATTGTTTCTATGAACCCTAATTTATCTTCCTTTGAGCTCTCTCGCCC

Query-      12015 TGTATCTCCTCTCACTCGCTCACTAGTTCCGTTCCGATCGACTAAACTAGTTCCCCGCTC
ATCEA4C371+   122 TGTATCTCCTCTCACTCGCTCACTAGTTCCGTTCCGATCGACTAAACTAGTTCCCCGCTC

Query-      11955 CATTTCTAGGGTTTCGCGCTCCATCTCCACCCCGAATAGTGAAACTGACAAGATCTCCGT
ATCEA4C371+   182 CATTTCTAGGGTTTCGCGCTCGATCTCCACCCCGAATAGTGAAACTGACAAGATCTCCGT

Query-      11895 TAAACCTGTTTACGTCCCGACGTCTCCCAATCGCGAACTCCGGACTCCTCACAGTGGGTA
ATCEA4C371+   242 TAAACCTGTTTACGTCCCGACGTCTCCCAATCGCGAACTCCGGACTCCTCACAGTGG
Synecho seq aligns from here

Query-      11835 AATTGATCCATTCCATTCCATTTCTTCTTCTTGTGTTTATTAAAGCTCCAATTTAG
ATCEA4C371+   299 -----
                ~~ 60 bp removed ~~

Query-      11715 *****TTTG
ATCEA4C371+   299 -----
PIR:T04448     1 -----

Query-      11655 GTGGCTCACCATTCGACGACTACTTTTGAATTGAGTTTTTGAAAAATGCAATTAAACAT
ATCEA4C371+   299 -----
PIR:T04448     1 :::::::::::::::::::: M Q F N I
                                     arab sequence which is incorrect

Query-      11595 CAGAGAGTTTTTTTTTTTATGGTTGATAACTTATTGTTTAACTTTTGAAAATGCAGATA
ATCEA4C371+   299 ----- ATA
PIR:T04448     6 R E F F F L W L I T Y C L T F E K C R Y

Query-      11535 CCATTTTCGATGGAACACCTCGGAAGTTCTTCGAGGGATGGTATTTTCAGGGTTTCCATCCC
ATCEA4C371+   302 CCATTTTCGATGGAACACCTCGGAAGTTCTTCGAGGGATGGTATTTTCAGGGTTTCCATCCC
PIR:T04448    26 H F D G T P R K F F E G W Y F S I P

```

Figure 31A

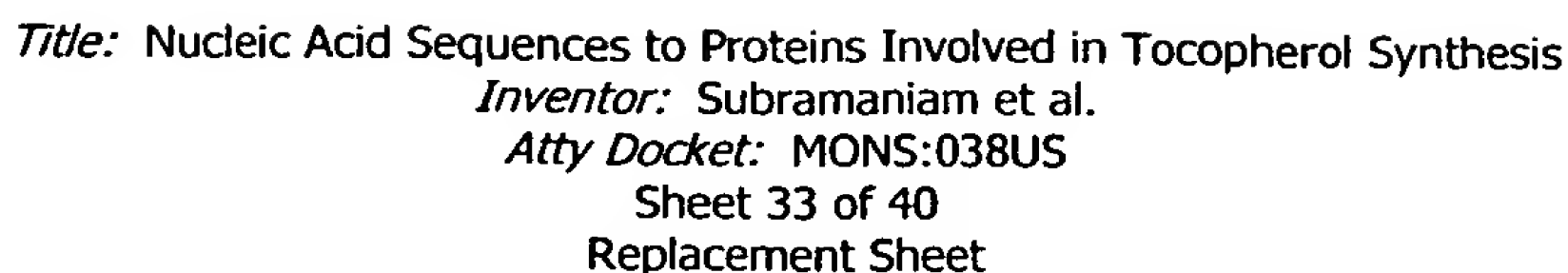


Figure 31B

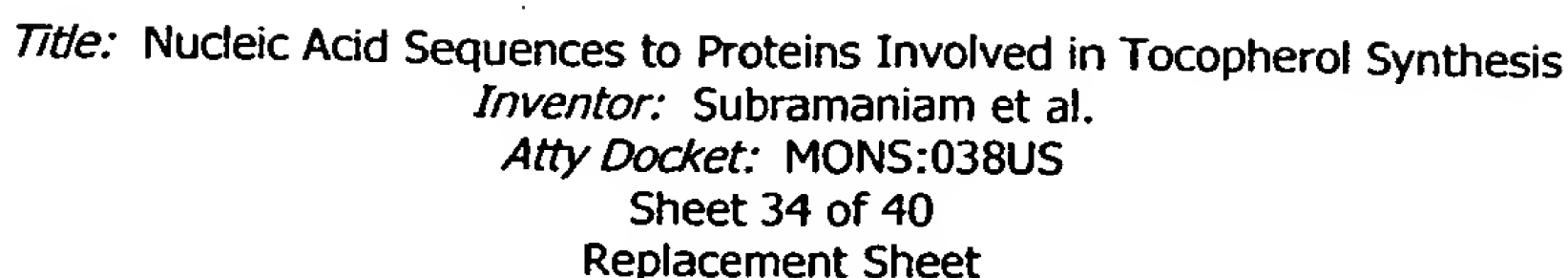


Figure 31C



Query- 9436 AAAGAGCTCAATGGCAGCAGTGGAGATAGGAGGAGGACCGTGGTTTGGGACATGGAAAGG
PIR:T04448 402 K S S M A A V E I G G G P W F G T W K G
GSDB:S:495- 307 aaagagctcaatggcaNcagtggagataggaggaggaccgtggtttgggacatggaaagg

Query- 9376 AGATACGAGCAACACGCCCGAGCTACTAAAACAGGCTCTTCAGGTCCCATTGGATCTTGA
PIR:T04448 422 D T S N T P E L L K Q A L Q V P L D L E
GSDB:S:495- 247 agatacgagcaacacgceccgagctactaaaacaggctcttcagggtcccattggatcttga

Query- 9316 AAGCGCCTTAGGTTTGGTCCCTTTCTTCAAGCCACCGGGTCTGTAA
(stop)
PIR:T04448 442 S A L G L V P F F K P P G L
GSDB:S:495- 187 aagcgccttaggtttggtccctttcttcaagccaccgggtctgtaacattgatgagtgtt
PIR:T04448 Exon 9522 9274 Confidence: 100 100

Query- 9256
PIR:T04448 456
GSDB:S:495- 127 ttgtttgttgatagagacccatgtgatgaatgaagccttagtcatgtcattgctagcttc

Query- 9196 ACTATTATGTATGTATGATTTTAGTTTCGTTTCGGTCTTGTGGTAAATGATACGGGCCAGT
GSDB:S:495- 67 actattatgtatgtatgatttttagttcgttcggtccttgtggtaaatagatacgggccagt

Query- 9136 GTAAAGTCTAGTTCAATAAAAGCCTTGAGTCGCATAATTTCAATTCAAATTGCATC
GSDB:S:495- 7 gtaaagt
GSDB:S:495- Exon 9450 9130 Confidence: 98 100

ATCEA4C37145_1 3063693/emb|CAA18584.1| 4.0e-43 (AL022537) putative protein
[Arabidopsis thaliana]

PIR:T04448 sPIR-T04448 shypothetical protein F4D11.30 - Arabidopsis thaliana;
g3063693|emb|CAA18584.1 (AL022537) putative protein [Arabidopsis thaliana]_F4D11.30

GSDB:S:4955486|AI995392|AI995392|701673779 A. thaliana, Columbia Col-0, inflorescence-
1 Arabidopsis thaliana cDNA clone 701673779, mRNA sequence.

Figure 31E

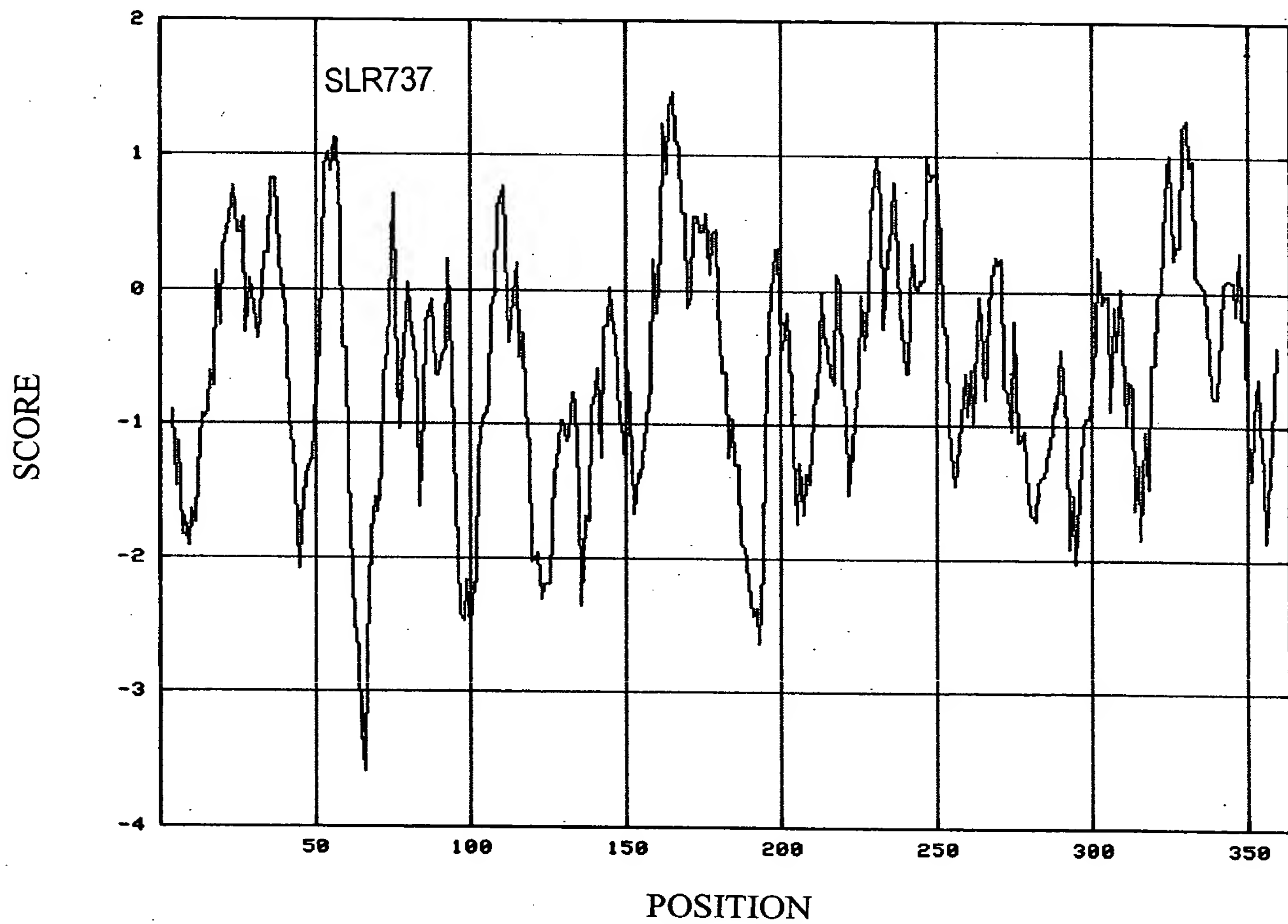


Figure 32

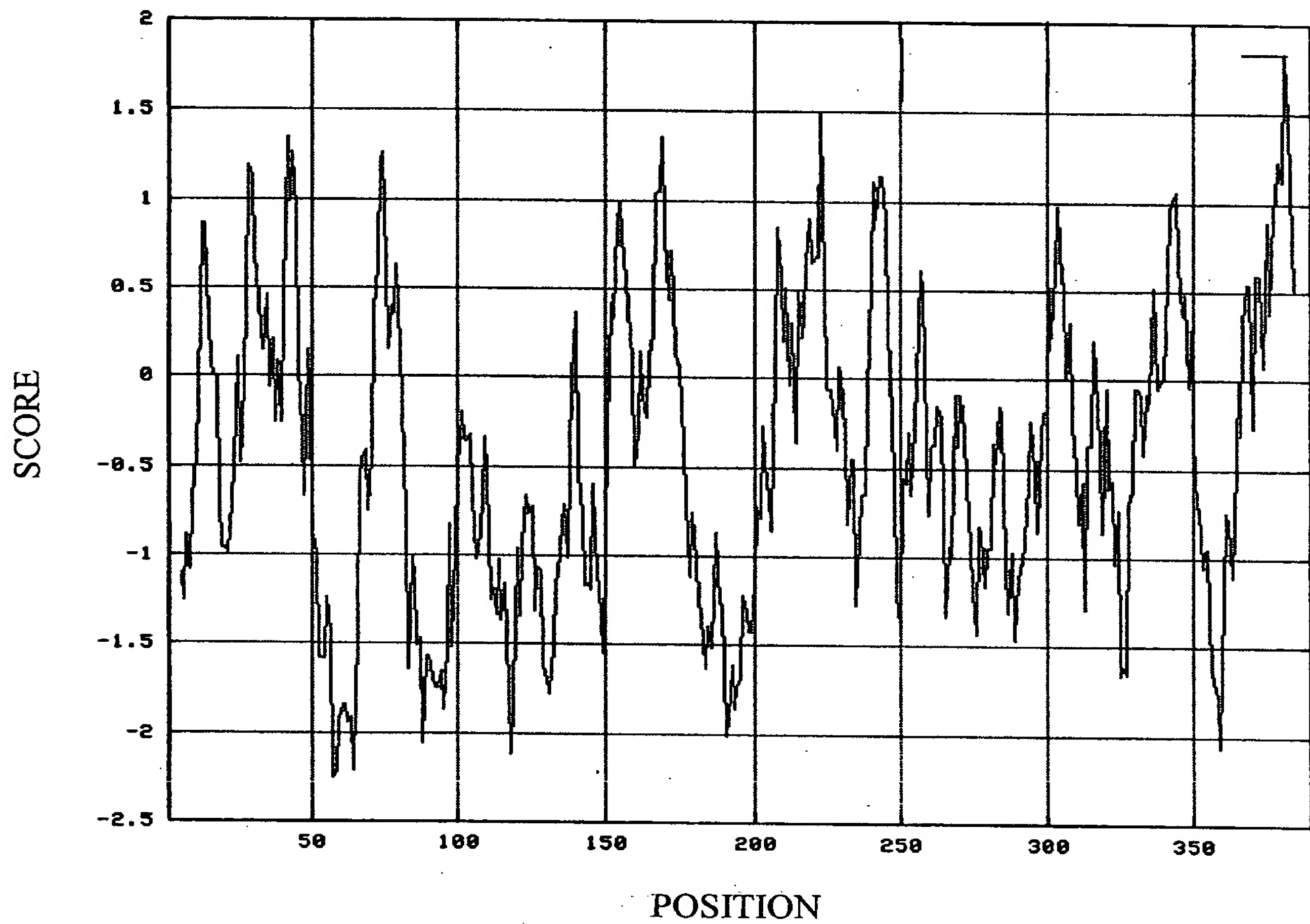


Figure 33

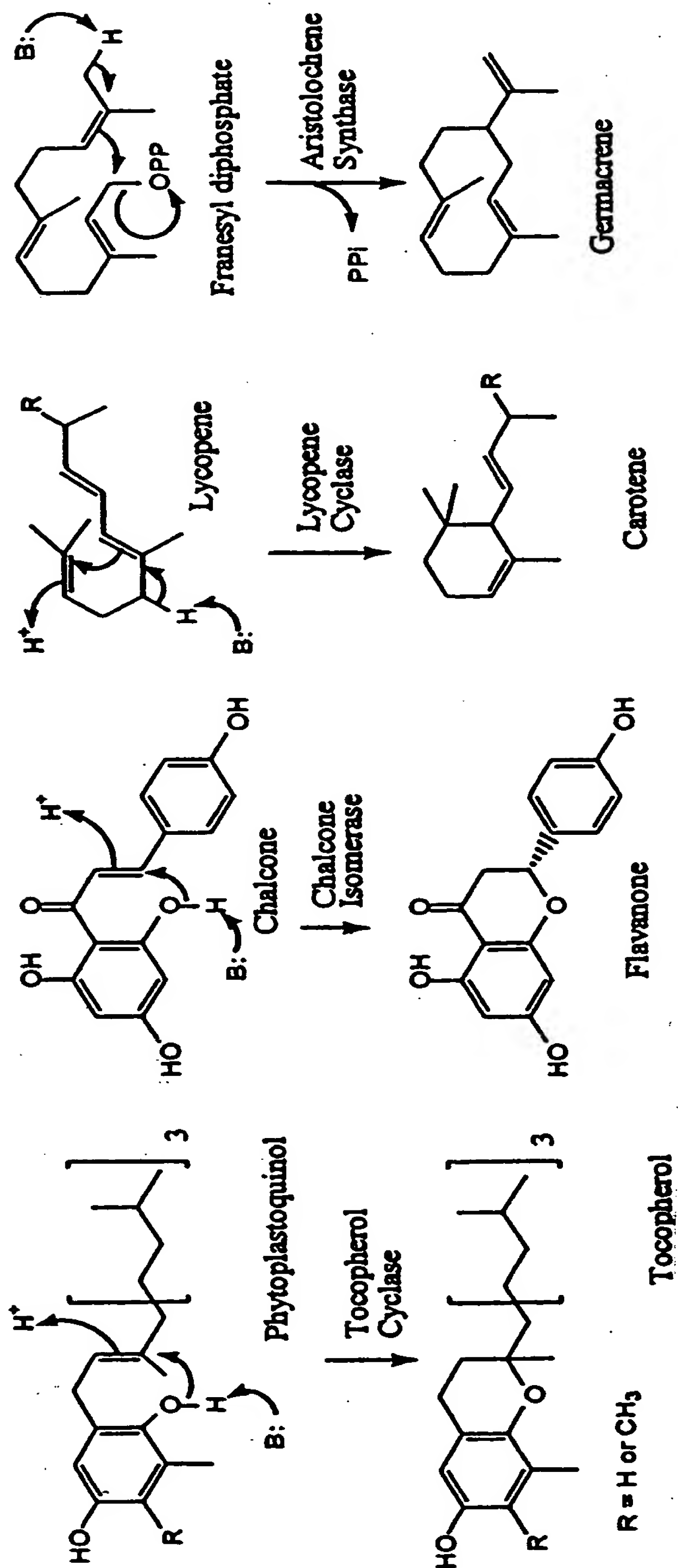


Figure 34



slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

-----M
MEIRSLIVSMNPNLSSFELSRPVSPLTRSLVPFRSTKLVPRISISRVSASI

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

KFP-----PHSGYHWQGS-PFFEGWYVRL
STPNSETDKISVKPVYVPTSPNRELRTPHSGYHFDGT
PRKFFEGWYFRVS

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

LPOSGESFAFMYSIENPASDHHYGGGAVQILGPATK---KQENQEDQLV
IPEKRESFCFMYSVENPAFRQSLSPLEVALYGPFRFTGVGAQILGANDKYL
MSSSNACASPSPPFA---VTKLHVDSV-

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

WRTFPSVKKFWASPRQFALG-HWGKCRDNRQ-AKPLLSEEFFATVKEGYQ
CQYEQDSHNFWGDRHELVLGNTFSAVPGAKAPNKEVPPEEFNRRVSEGFQ
--TFVPSVKSPASSNPLFLG-GAGVRGLDIQ-GK-----FVIFTVIGVY

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

IHQNHQGGQIIHGDR-----HCRWQFTVEPEVTWGS
PNRFPFRATAGW
ATPFWHQGHICDDGRTDYAETVKSARWEYSTRPVY
GWDVGAKQKSTAGW
LEGNVPSLSV-----KWKGKTTEELTESIPFFREIVTGAF

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

LSFLPLFDPGWQILLAQGRAHWLKWQREQYEFDHALVYAEKNWGH
SFPS
PAAFPVFEPHWQICMAGGLSTGWIEWGGERFEFRDAPSYSEKNWGGG
FPR
EKFIKVT-----M-----KLPLTGQYSEKVTENC

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

RFWLQANYFPDHPG-LSVTAAGGERIVLGRPE---EVALIGLHHQGNFY
KFWVQCNVFEGATGEVALTAGGGLRQLPGLTETYENAALVCVHYDG
KMY
VAIWKQLGLYTDCEA-KAV-----EKFLIEFKE---ET-----

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

EFGPGHGTVTWQVAPWGRWOLKASNDRYWVKLSGKTDKKGSLVHTP-TAQ
EFVPWNGVVRWEMSPWGYWYITAENENHVVELEARTNEAGTPLRAPTEV
-FPPG-SSILFALSPTGSLTVAFSKDDS-IPETGIAVIENKLLAEA-VLE

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

GLQLNCRDTRGYLYLQLGSVGHG-----LIVQGETDTAGLEVGG-----
GLATACRDSCYGELKLQIWERLYDGSKGKVILETKSSMAAVEIGGGPWFG
--SIIGKNGVSPGTRLSVAERLSQ-----LMMKNKDEKEVSDHSL-----

slr1737_SYNSP_S74814_
slr1737_ARATH_T04448_
CFI_ARATH_P41088_

----DWGLTEENLSKKT-----VPF-----
TWKGDTSENTPELLKQALQVPLDLESALGLVPFFKPPGL
----EEKLAKEN-----

Figure 35